Proteins detected under conventional growth conditions (BHI supplemented with 5% FCS) in B. hyodysenteriae P7455

Accession	Protein	MW [kDa]	pI	Scores	Peptides			SC
Bhyoa7455_0047	ModA, ABC-type molybdate transport system, periplasmic component	28.5	4.7	226.2	4	4		28.9
Bhyoa7455_0055	ABC-type oligopeptide transport system, periplasmic component	60.7	4.7	1803.0	31	27	22	60.7
Bhyoa7455_0062	30S ribosomal protein S2	29.6	5.0	317.5	7	6	6	45.9
Bhyoa7455_0063	elongation factor Ts	31.2	5.2	320.7	8	7		33.1
Bhyoa7455_0064	TPR domain-containing protein	52.5	5.1	891.3	17	16	15	40.6
Bhyoa7455_0088	chemotaxis response regulator CheY	13.5	7.6	240.6	5	5		51.6
Bhyoa7455_0090	putative methyl-accepting chemotaxis protein	74.0	4.4	110.3	4	4	3	7.2
Bhyoa7455_0100	ABC-type uncharacterized transport system	61.4	9.4	292.8	6	4		21.4
Bhyoa7455_0115	putative dynein heavy chain	42.4	4.5	968.9	17	14	9	45.1
Bhyoa7455_0127	aminodeoxychorismate lyase	38.1	9.2	169.6	4	2		20.9
Bhyoa7455_0133	methyl-accepting chemotaxis protein McpB	75.7	4.9	282.9	5	5	3	12.9
Bhyoa7455_0137	hypothetical protein	20.9	4.8	456.3	8	8	8	47.2
Bhyoa7455_0170	ankyrin repeat-containing protein	71.0	4.6	242.2	6	6		12.6
Bhyoa7455_0171	solute binding protein-like protein	97.5	4.8	828.1	13	13	8	20.7
Bhyoa7455_0174	phosphate ABC transporter, phosphate-binding protein	27.5	4.3	1018.7	14	14	10	58.6
Bhyoa7455_0180	ABC-type uncharacterized transport system, periplasmic component	32.9	4.4	906.7	15	15	10	76.3
Bhyoa7455_0181	hypothetical protein	19.8	5.8	267.4	5	5		37.1
Bhyoa7455_0182	**hypothetical protein**	**18.6**	**4.7**	**392.0**	**6**	**6**	**6**	**49.1**
Bhyoa7455_0194	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit	48.2	9.9	202.1	3	3	2	10.0
Bhyoa7455_0195	biotin/lipoyl attachment domain-containing protein	64.2	5.7	1777.4	33	31	29	64.5
Bhyoa7455_0207	peptidase	31.7	6.0	169.4	4	4		20.0
Bhyoa7455_0232	**hypothetical protein**	**51.4**	**4.8**	**1293.4**	**22**	**20**	**19**	**55.3**

Bhyoa7455_0250	ABC-type nitrate/sulfonate/bicarbonate transport system	37.2	4.5	888.0	15	13	8	62.0
Bhyoa7455_0260	hypothetical protein	19.7	5.5	218.9	3	3		23.8
Bhyoa7455_0271	hypothetical protein	24.5	9.2	198.2	3	3	3	16.7
Bhyoa7455_0294	**hypothetical protein**	**57.0**	**4.1**	**193.3**	**5**	**5**		**9.5**
Bhyoa7455_0295	**hypothetical protein**	**38.2**	**4.1**	**415.2**	**7**	**7**	**5**	**28.3**
Bhyoa7455_0299	pts system, N-acetylglucosamine-specific iibc component	50.6	8.7	545.7	11	10	7	27.6
Bhyoa7455_0301	response regulatory protein (atoC)	51.1	5.5	103.1	5	3		16.9
Bhyoa7455_0311	**hypothetical protein**	**73.8**	**5.1**	**726.9**	**13**	**11**	**4**	**30.1**
Bhyoa7455_0335	hypothetical protein	18.8	5.1	128.4	2	2		21.7
Bhyoa7455_0336	putative positive regulator of sigma E, RseC/MucC	15.8	9.3	324.0	8	8	8	45.7
Bhyoa7455_0338	TPR domain-containing protein	53.6	6.0	1072.1	20	20	14	43.7
Bhyoa7455_0340	hypothetical protein	40.0	5.6	327.8	6	4		23.4
Bhyoa7455_0341	**hypothetical protein**	**38.1**	**4.8**	**1321.9**	**27**	**23**	**15**	**55.3**
Bhyoa7455_0347	putative chaperone protein DnaJ	11.2	10.0	145.6	2	2	2	27.1
Bhyoa7455_0367	**galactose/glucose-binding protein**	**38.2**	**4.7**	**4876.7**	**86**	**73**	**50**	**75.7**
Bhyoa7455_0368	galactose/methyl galaxtoside transporter ATP-binding protein	56.1	9.1	789.1	15	10		35.7
Bhyoa7455_0369	beta-methylgalactoside transporter inner membrane component	36.0	0.0	135.0	3	2	2	5.0
Bhyoa7455_0382	**OppA, ABC-type oligopeptide transport system, periplasmic component**	**60.8**	**4.9**	**1207.1**	**20**	**17**	**12**	**43.3**
Bhyoa7455_0387	binding-protein-dependent transport system, membrane component	35.5	9.8	177.6	3	3	2	12.2
Bhyoa7455_0404	OppA, ABC-type oligopeptide transport system, periplasmic component	59.4	4.6	997.3	20	16	7	45.0
Bhyoa7455_0408	**hypothetical protein**	**41.0**	**5.1**	**296.3**	**7**	**5**	**3**	**36.8**
Bhyoa7455_0418	50S ribosomal protein L25/general stress protein Ctc	21.9	5.6	464.5	9	9	7	57.7
Bhyoa7455_0424	DH oxidase	50.1	6.1	866.4	19	13	11	54.2
Bhyoa7455_0446	periplasmic ATP/GTP-binding protein	32.7	4.3	252.9	5	5	5	22.0
Bhyoa7455_0448	hypothetical protein	20.3	4.4	345.6	7	6	4	30.6

Bhyoa7455_0459	hypothetical protein	30.5	6.0	419.0	6	6	5	31.6
Bhyoa7455_0460	hypothetical protein	30.1	9.7	212.1	5	52		21.2
Bhyoa7455_0473	ankyrin repeat-containing protein	15.2	5.4	336.0	6	6	4	52.6
Bhyoa7455_0477	hypothetical protein	68.1	5.7	105.1	4	3	3	6.3
Bhyoa7455_0483	metal dependent amidohydrolase	63.9	5.0	665.6	12	10	8	27.7
Bhyoa7455_0486	phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	31.2	5.4	509.5	8	8	5	39.7
Bhyoa7455_0487	hypothetical protein	15.2	0.0	413.6	5	5	5	43.4
Bhyoa7455_0517	TRAP transporter solute receptor, TAXI family	34.4	4.5	1035.0	19	17	14	54.4
Bhyoa7455_0523	carbon starvation protein CstA	58.6	9.7	428.5	9	6	6	16.9
Bhyoa7455_0537	putative UshA protein; putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	57.2	4.8	541.4	12	9	6	27.7
Bhyoa7455_0538	spermidine/putrescine transport ATP-binding protein PotA	45.3	4.6	548.0	8	8	4	35.8
Bhyoa7455_0550	hypothetical protein	27.5	9.6	128.0	4	3		18.3
Bhyoa7455_0552	**hypothetical protein**	**38.4**	**8.8**	**102.9**	**3**	**3**		**13.5**
Bhyoa7455_0574	**putative flagellar filament outer layer protein FlaA**	**27.6**	**4.6**	**105.7**	**4**	**3**		**34.0**
Bhyoa7455_0585	50S ribosomal protein L7/L12	13.3	4.8	244.5	4	4		60.9
Bhyoa7455_0590	pututative preprotein translocase subunit SecE	12.1	10.4	120.3	4	4	3	14.2
Bhyoa7455_0612	hypothetical protein	24.7	4.8	267.7	5	4	4	28.9
Bhyoa7455_0615	hypothetical protein	18.9	4.8	113.9	2	2	2	18.4
Bhyoa7455_0619	invasin; Opacity protein-like surface antigens	25.0	9.3	113.5	3	2		20.5
Bhyoa7455_0623	hypothetical protein	24.7	5.3	153.5	3	3		33.2
Bhyoa7455_0629	PilZ domain containing protein	28.9	5.1	143.2	3	3		17.1
Bhyoa7455_0678	ThiJ/PfpI domain-containing protein	20.0	4.8	107.8	3	3		44.0
Bhyoa7455_0691	outer membrane protein	100.3	6.7	1140.9	18	18	15	24.4
Bhyoa7455_0711	membrane-bound proton-translocating pyrophosphatase	79.8	5.9	303.0	5	4		9.4
Bhyoa7455_0730	chemotaxis protein CheY	15.6	9.2	105.6	3	2	2	21.6
Bhyoa7455_0741	isoleucyl-tRNA synthetase	106.0	5.8	152.4	4	3		6.4
Bhyoa7455_0756	methyl-accepting chemotaxis-like domains (chemotaxis sensory transducer)	62.4	4.5	135.8	3	3		11.8

Bhyoa7455_0765	GltP, Na+/H+-dicarboxylate symporter	40.2	9.2	189.6	3	3		10.3
Bhyoa7455_0772	hypothetical protein	58.9	8.9	169.0	3	3		14.7
Bhyoa7455_0792	alkaline phosphatase III	57.7	4.8	1380.5	20	18	17	60.0
Bhyoa7455_0816	triosephosphate isomerase	27.6	5.7	161.2	2	2		19.8
Bhyoa7455_0825	hypothetical protein	51.2	8.8	593.1	11	11	9	30.8
Bhyoa7455_0856	**UshA, 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase**	**68.3**	**4.7**	**386.7**	**9**	**8**	**7**	**21.9**
Bhyoa7455_0865	hypothetical protein	27.8	5.1	107.9	2	2		9.6
Bhyoa7455_0888	-	31.9	7.6	122.0	4	3		13.3
Bhyoa7455_0934	**hypothetical protein**	**47.8**	**5.9**	**75.8**	**3**	**3**		**7.9**
Bhyoa7455_0941	peptidase	47.1	5.3	115.5	3	3	3	7.1
Bhyoa7455_0944	hypothetical protein	35.0	4.9	359.5	6	3		28.6
Bhyoa7455_0946	non-heme iron-containing ferritin	20.9	4.9	190.4	4	3	2	25.0
Bhyoa7455_0958	hypothetical protein	18.0	4.9	143.4	4	4		38.7
Bhyoa7455_0964	purine-binding chemotaxis protein	17.9	4.3	200.0	3	3		31.4
Bhyoa7455_0980	hypothetical protein	33.4	5.0	185.8	4	4	3	22.1
Bhyoa7455_1004	extracellular solute-binding protein, family 5	61.7	4.8	218.8	4	4	4	9.2
Bhyoa7455_1009	ABC transporter, transmembrane region	73.2	9.3	163.2	3	3		10.6
Bhyoa7455_1020	chaperonin GroEL	58.2	4.9	1015.5	18	15	9	53.2
Bhyoa7455_1029	**hypothetical protein**	**22.2**	**5.2**	**196.8**	**3**	**2**	**2**	**15.4**
Bhyoa7455_1042	putative Na+/phosphate symporter	61.9	6.3	305.6	7	6	3	20.0
Bhyoa7455_1049	methyl-accepting chemotaxis protein McpB	68.3	4.7	158.2	5	4	3	8.0
Bhyoa7455_1071	3-hydroxybutyryl-CoA dehydratase	29.9	8.8	409.6	8	3	8	36.8
Bhyoa7455_1072	3-hydroxybutyryl-CoA dehydratase	27.7	5.4	676.4	10	10	8	48.4
Bhyoa7455_1073	acetyl-CoA acetyltransferase	40.9	8.8	356.1	9	8	5	35.2
Bhyoa7455_1085	PTS system, fructose subfamily, IIC subunit	17.3	7.7	54.3	3	3		18.2
Bhyoa7455_1098	**acetyltransferase, GT family**	**20.9**	**5.2**	**192.4**	**7**	**5**		**5.7**
Bhyoa7455_1150	peroxiredoxin family, thiol peroxidase	17.9	5.2	730.2	13	12	9	89.1
Bhyoa7455_1163	extracellular solute-binding protein, family 5	51.8	4.9	108.7	3	3		10.0

Bhyoa7455_1164	extracellular solute-binding protein, family 5	60.8	5.2	678.3	16	13	11	38.5
Bhyoa7455_1167	putative methyl-accepting chemotaxis protein B	75.7	4.6	226.3	6	4	3	10.2
Bhyoa7455_1180	hypothetical protein	38.1	10.6	292.6	5	4	4	12.5
Bhyoa7455_1188	**ankyrin repeat-containing protein**	**62.1**	**4.5**	**63.5**	**2**	**2**		**6.6**
Bhyoa7455_1206	Heat shock protein	17.2	4.1	560.1	8	7	5	37.4
Bhyoa7455_1239	Signal recognition particle GTPase	35.4	9.1	1172.8	16	16	15	44.0
Bhyoa7455_1247	putative cytidylate kinase	23.4	6.5	101.4	3	2	2	19.3
Bhyoa7455_1252	NifS, Cysteine sulfinate desulfinase/cysteine desulfurase-like enzyme	42.9	5.9	76.0	3	3		9.3
Bhyoa7455_1272	hypothetical protein	26.8	4.9	1260.0	20	19	16	58.1
Bhyoa7455_1290	ankyrin repeat-containing protein	61.1	4.3	1743.9	27	26	25	55.7
Bhyoa7455_1308	integral membrane transport protein	46.1	5.4	209.0	5	5	4	15.1
Bhyoa7455_1328	electron transport complex protein	46.8	8.6	1700.5	28	27	22	66.0
Bhyoa7455_1329	putative electron transport complex	39.4	9.9	83.6	3	3	3	9.6
Bhyoa7455_1330	putative electron transport complex	19.9	4.5	805.7	15	14	9	62.3
Bhyoa7455_1338	phosphoglycerate kinase	44.1	5.8	137.4	3	3		13.6
Bhyoa7455_1339	glyceraldehyde-3-phosphate dehydrogenase	38.1	7.8	758.8	13	13	8	49.6
Bhyoa7455_1340	glutamyl-tRNA(Gln) amidotransferase, B subunit	54.5	6.0	89.6	4	4	4	13.5
Bhyoa7455_1359	galactose/glucose-binding protein	37.8	4.4	1049.2	18	12	11	68.1
Bhyoa7455_1360	galactose/glucose-binding protein	38.7	9.4	107.5	5	4	3	10.7
Bhyoa7455_1361	3-dehydroquinate synthetase	39.9	6.1	84.8	4	4		11.7
Bhyoa7455_1371	extracellular solute-binding protein, family 3	30.1	5.3	1304.1	19	18	15	63.9
Bhyoa7455_1375	periplasmic-iron-binding protein BitB	38.2	4.7	579.3	11	8	5	45.7
Bhyoa7455_1376	periplasmic-iron-binding protein BitB	39.0	4.6	261.6	4	4	2	27.4
Bhyoa7455_1412	hypothetical protein	63.4	7.5	192.4	7	6	3	10.1
Bhyoa7455_1415	thiol-disulfide interchange protein DsbD-like protein	31.2	4.6	182.0	4	4		18.1
Bhyoa7455_1416	thiol-disulfide interchange protein DsbD-like protein	31.6	5.4	384.3	8	8	3	34.9

Bhyoa7455_1427	hypothetical protein	14.9	4.5	317.0	4	4	4	22.9
Bhyoa7455_1437	hypothetical protein	27.5	5.0	293.8	5	3	5	25.4
Bhyoa7455_1443	**hypothetical protein**	**60.7**	**5.9**	**1028.9**	**21**	**12**	**16**	**43.9**
Bhyoa7455_1461	Predicted membrane protein	23.2	10.6	89.8	2	2	2	11.6
Bhyoa7455_1470	hypothetical protein	19.3	5.2	680.5	14	13	10	68.4
Bhyoa7455_1479	BmpB, outer membrane lipoprotein	29.7	4.3	772.8	12	12	11	36.9
Bhyoa7455_1483	transcriptional regulator	32.3	5.8	68.3	4	4		14.7
Bhyoa7455_1502	acyl-CoA synthetase	62.2	6.6	272.2	6	5	4	18.7
Bhyoa7455_1505	dinB family protein	32.5	10.0	48.1	3	3		10.8
Bhyoa7455_1510	TPR domain-containing protein	20.2	4.9	140.5	3	2		26.0
Bhyoa7455_1522	Phosphopyruvate hydratase	47.0	4.8	929.2	15	13	8	49.7
Bhyoa7455_1535	PTS system, IIa component	16.3	4.2	53.7	3	3		14.8
Bhyoa7455_1536	amino acid-binding protein	28.6	4.9	237.0	4	4		17.3
Bhyoa7455_1543	electron transfer flavoprotein beta subunit	28.6	5.8	439.8	8	8	4	56.3
Bhyoa7455_1544	acyl-CoA dehydrogenase	40.0	6.1	256.8	9	6	3	24.0
B.hyoa7455_1547	V-type ATP synthase subunit A	65.1	5.0	296.2	6	5	2	20.1
B.hyoa7455_1548	V-type ATP synthase subunit B	48.4	4.9	102.2	2	2	2	7.7
B.hyoa7455_1550	putative V-type ATP synthase subunit I	68.7	6.1	516.4	11	8	8	19.1
B.hyoa7455_1560	hypothetical protein	43.1	5.1	221.3	5	5	3	19.4
Bhyoa7455_1566	hypothetical protein	39.6	5.6	57.6	2	2	2	10.3
Bhyoa7455_1583	hypothetical protein	35.6	4.8	1974.9	36	31	29	84.5
Bhyoa7455_1593	TPR domain-containing protein	77.5	5.2	218.1	4	3		10.9
Bhyoa7455_1603	OmpA family protein	25.2	9.6	106.8	2	2		9.5
Bhyoa7455_1604	hypothetical protein	26.2	9.3	120.4	3	3		20.3
Bhyoa7455_1605	**hypothetical protein**	**33.6**	**9.0**	**127.6**	**3**	**3**		**12.0**
Bhyoa7455_1606	hypothetical protein	17.5	4.4	136.0	4	4		42.4

Bhyoa7455_1610	elongation factor G	75.3	5.1	315.2	8	7	6	20.9
Bhyoa7455_1611	elongation factor Tu	44.4	5.8	1424.2	24	23	17	58.8
Bhyoa7455_1626	30S ribosomal protein S8	14.9	9.7	262.7	5	5		45.9
Bhyoa7455_1627	50S ribosomal protein L6	21.0	10.0	189.6	4	4		34.8
B.hyoa7455_1628	50S ribosomal protein L18	13.2	10.6	91.8	2	2		16.9
Bhyoa7455_1632	preprotein translocase subunit SecY	49.2	10.2	85.4	3	3		15.7
Bhyoa7455_1642	putative lipid A disaccharide synthase; LpxB	42.5	9.4	66.6	3	3		11.7
Bhyoa7455_1662	iron-containing alcohol dehydrogenase	42.0	5.5	96.4	4	4	4	19.4
Bhyoa7455_1674	extracellular solute-binding protein, family 5	59.4	4.6	1447.7	27	23	17	54.7
Bhyoa7455_1675	hypothetical protein	11.8	6.1	312.0	7	7	5	68.6
Bhyoa7455_1684	TPR domain-containing protein	68.3	5.1	209.8	9	5	4	9.6
Bhyoa7455_1686	**hypothetical protein**	**15.5**	**9.5**	**163.5**	**2**	**2**	**2**	**18.6**
Bhyoa7455_1693	OmpA family protein	23.9	4.6	479.7	8	8	6	59.6
Bhyoa7455_1708	SoxR-reducing system protein RsxE	23.4	10.0	152.4	2	2	2	5.0
Bhyoa7455_1709	RnfA, Predicted DH:ubiquinone oxidoreductase, subunit RnfA	21.1	9.4	128.1	2	2	2	5.7
Bhyoa7455_1710	ferredoxin	29.6	9.4	465.4	10	9	4	45.7
Bhyoa7455_1717	MiaB-like tRNA modifying enzyme	48.1	9.3	113.6	4	4		5.3
Bhyoa7455_1718	Cell division protein FtsZ	76.8	4.7	87.8	3	3		5.1
Bhyoa7455_1737	aspartate aminotransferase	45.8	5.8	266.0	5	4		19.1
Bhyoa7455_1743	**hypothetical protein**	**65.4**	**4.2**	**221.0**	**4**	**4**		**13.0**
Bhyoa7455_1745	hypothetical protein	23.0	4.7	101.0	2	2		11.1
Bhyoa7455_1753	OmpR	26.2	4.9	123.2	3	3		22.4
Bhyoa7455_1770	**hypothetical protein**	**59.1**	**4.8**	**514.8**	**9**	**9**	**9**	**20.4**
Bhyoa7455_1771	**hypothetical protein**	**58.0**	**4.9**	**747.2**	**12**	**11**	**10**	**24.6**
Bhyoa7455_1772	hypothetical protein	30.7	4.5	1174.1	20	18	13	49.3
Bhyoa7455_1780	ABC transporter substrate binding protein	35.1	4.6	1122.4	17	14	11	55.3

Bhyoa7455_1783	**variable surface protein A**	**38.1**	**4.5**	**684.2**	**10**	**9**	**7**	**37.9**
Bhyoa7455_1785	periplasmic solute binding protein	32.3	4.6	128.4	3	3		15.3
Bhyoa7455_1808	hypothetical protein	27.9	8.7	164.3	4	3		19.4
Bhyoa7455_1821	pyruvate oxireductase	38.0	9.4	653.1	12	12	8	42.3
Bhyoa7455_1822	pyruvate ferredoxin oxireductase	82.9	6.2	1083.2	23	22	9	44.0
Bhyoa7455_1832	hypothetical protein	23.5	5.4	344.8	5	5	3	36.6
Bhyoa7455_1866	hypothetical protein	88.0	5.1	154.1	5	3		6.1
Bhyoa7455_1884	Flagellar Motor Protein	27.8	4.8	318.5	5	4	3	21.3
Bhyoa7455_1893	extracellular solute-binding protein, family 5	61.8	4.9	3016.1	58	54	45	67.9
Bhyoa7455_1913	hypothetical protein	28.1	4.6	450.9	9	9	4	51.6
Bhyoa7455_1918	periplasmic flagellar filament protein FlaB3	30.1	5.2	78.4	3	3		15.1
Bhyoa7455_1920	Zn dependant metalloprotease	25.8	9.1	228.0	4	4	2	20.3
Bhyoa7455_1930	hypothetical protein	39.4	4.9	199.9	6	5	2	21.0
Bhyoa7455_1946	hypothetical protein	28.6	4.9	357.0	6	6	4	31.2
Bhyoa7455_1947	hypothetical protein	27.2	9.2	443.9	8	7	7	19.8
Bhyoa7455_1957	hypothetical protein	40.4	5.7	255.4	5	4		20.5
Bhyoa7455_1969	hypothetical protein	18.8	5.2	392.1	7	7	6	48.5
Bhyoa7455_1981	hypothetical protein	15.3	4.3	248.9	3	3	3	38.6
Bhyoa7455_2024	hypothetical protein	14.8	4.8	282.5	6	6		59.1
Bhyoa7455_2025	hypothetical protein	18.8	4.5	216.9	3	3	2	24.2
Bhyoa7455_2046	hypothetical protein	39.9	4.4	1002.0	15	15	12	46.2
Bhyoa7455_2064	3-oxoacyl-ACP (acyl carrier protein) synthase II	44.5	6.1	161.4	4	4	4	17.5
Bhyoa7455_2073	**hypothetical protein**	**107.0**	**6.4**	**342.2**	**8**	**7**		**10.8**
Bhyoa7455_2078	**AMP-activated protein kinase (AMPK) beta subunit glycogen binding domain (GBD)**	**29.4**	**4.8**	**245.6**	**5**	**5**		**31.7**
Bhyoa7455_2088	methyl-accepting chemotaxis protein McpB	61.3	4.8	147.6	3	2		6.9
Bhyoa7455_2091	Phosphoribosylamidoimidazole-succinocarboxamide synthase	27.3	6.0	109.6	2	2		13.4
Bhyoa7455_2097	alpha-amylase 1 (1,4-alpha-D-glucan glucanohydrolase)	82.5	5.4	170.5	8	6	4	13.6
Bhyoa7455_2102	hypothetical protein	25.3	4.9	138.8	3	2		23.5

Bhyoa7455_2111	ankyrin repeat-containing protein	42.6	4.6	294.8	7	6		32.5
Bhyoa7455_2168	Rieske (2Fe-2S) domain protein	38.1	9.7	434.9	15	14	14	10.2
Bhyoa7455_2176	basic membrane lipoprotein	38.6	4.6	745.3	12	11	7	51.4
Bhyoa7455_2177	**basic membrane lipoprotein**	**36.9**	**4.6**	**1301.6**	**17**	**16**	**14**	**55.6**
Bhyoa7455_2185	hypothetical protein	10.0	5.4	287.5	5	5	5	47.7
Bhyoa7455_2192	extracellular solute-binding protein, family 3	29.2	4.5	2422.5	32	31	29	77.4
Bhyoa7455_2198	hypothetical protein	18.4	9.3	536.5	10	10	9	58.3
Bhyoa7455_2210	ankyrin repeat-containing protein	40.4	4.3	518.2	10	10	2	42.1
Bhyoa7455_2214	lipoprotein involved with copper homeostasis and adhesion	14.5	4.0	279.6	4	4	4	26.2
Bhyoa7455_2217	bifunctional methionine sulfoxide reductase	23.3	6.6	120.3	3	3		22.8
Bhyoa7455_2224	**hypothetical protein**	**28.2**	**5.5**	**293.6**	**6**	**5**	**2**	**22.8**
Bhyoa7455_2234	phosphoenolpyruvate carboxykinase (GTP)	66.6	5.8	617.7	11	9	4	28.8
Bhyoa7455_2239	oligopeptide ABC transporter periplasmic subunit	61.3	5.9	812.3	16	13	9	35.7
Bhyoa7455_2247	hypothetical protein	25.1	4.6	451.5	10	7		43.0
Bhyoa7455_2257	hypothetical protein	23.3	6.4	531.4	8	8	7	44.4
Bhyoa7455_2258	hypothetical protein	21.1	6.1	357.7	7	7	4	44.8
Bhyoa7455_2288	**hypothetical protein**	**15.4**	**8.9**	**109.3**	**4**	**4**	**4**	**30.5**
Bhyoa7455_2320	extracellular solute-binding protein, family 3	30.4	4.7	1285.6	18	17	15	52.7
Bhyoa7455_2321	extracellular solute-binding protein, family 3	31.1	4.8	848.5	13	12	8	56.0
Bhyoa7455_2322	Leucine-rich repeat containing protein	32.6	9.2	65.5	3	3		9.0
Bhyoa7455_2325	endoribonuclease	13.9	5.3	139.6	2	2		22.0
Bhyoa7455_2337	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	39.3	7.7	102.8	3	3		7.0
Bhyoa7455_2344	hypothetical protein	60.5	7.8	209.0	5	4	4	10.6
Bhyoa7455_2347	argininosuccinate lyase	45.6	5.6	230.8	6	6	3	26.6
Bhyoa7455_2361	**variable surface protein - VspE**	**40.5**	**6.5**	**1301.1**	**16**	**15**	**13**	**43.2**
Bhyoa7455_2368	SpoIIAA, Anti-anti-sigma regulatory factor	12.2	5.2	181.9	2	2		26.4
Bhyoa7455_2371	putative methyl-accepting chemotaxis protein B	67.4	4.9	208.4	5	4		14.3

Bhyoa7455_2378	methyl-accepting chemotaxis protein McpA	67.5	4.6	331.0	7	8	7	15.1
Bhyoa7455_2380	hypothetical protein	47.7	4.2	105.6	2	2		5.1
Bhyoa7455_2381	extracellular solute-binding protein, family 5	62.3	5.0	1079.6	18	17	9	50.7
Bhyoa7455_2382	extracellular solute-binding protein, family 5	59.4	4.8	1552.3	23	20	19	53.2
Bhyoa7455_2383	extracellular solute-binding protein, family 5	60.3	4.7	710.8	14	12	7	39.5
Bhyoa7455_2404	fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB , and IIA components	77.4	6.1	478.0	9	8	4	16.8
Bhyoa7455_2408	hypothetical protein	55.9	9.2	556.1	11	7	6	29.9
Bhyoa7455_2411	rubrerythrin	20.6	5.9	390.0	6	6	4	59.6
Bhyoa7455_2412	superoxide dismutase	22.1	6.3	338.6	6	6	3	52.6
Bhyoa7455_2429	**hypothetical protein**	**143.4**	**6.7**	**186.3**	**4**	**4**		**5.1**
Bhyoa7455_2452	extracellular solute-binding protein, family 5	59.8	4.6	1771.9	34	28	19	57.0
Bhyoa7455_2454	hypothetical protein	37.9	4.6	539.4	12	9	3	37.8
Bhyoa7455_2455	TPR domain-containing protein	26.2	5.5	140.2	3	3		13.9
Bhyoa7455_2465	putative preprotein translocase subunit	15.8	9.5	681.9	10	10	8	42.7
Bhyoa7455_2466	preprotein translocase subunit SecD	55.1	5.0	730.2	13	12	11	28.4
Bhyoa7455_2467	preprotein translocase	34.3	8.8	278.4	4	3	3	13.7
Bhyoa7455_2477	putative flagellar basal body-associated protein	20.2	4.6	1028.9	15	15	14	60.2
Bhyoa7455_2517	hypothetical protein	50.5	5.2	263.8	6	4		25.8
Bhyoa7455_2523	hypothetical protein	37.5	5.8	66.5	3	3		5.4
Bhyoa7455_2532	methyl-accepting chemotaxis protein McpB	66.0	4.6	178.0	5	3		8.5
Bhyoa7455_2544	hypothetical protein	88.4	4.6	220.6	6	5	3	15.6
Bhyoa7455_2553	ABC-type oligopeptide transport system, periplasmic component	59.8	5.1	1696.0	31	26	21	61.6
Bhyoa7455_2554	ABC-type oligopeptide transport system, periplasmic component	61.2	5.5	168.1	4	2	2	11.8
Bhyoa7455_2567	periplasmic-iron-binding protein BitB	15.4	4.7	178.3	2	2		44.6
Bhyoa7455_2610	hypothetical protein	22.0	9.1	251.4	4	4		25.9
Bhyoa7455_2618	basic membrane lipoprotein	16.9	4.2	305.1	6	5	4	52.6
Bhyoa7455_263	**putative inversin protein alternative isoform**	**64.3**	**4.2**	**339.7**	**6**	**4**	**4**	**17.5**

4								
Bhyoa7455_2645	sodium:alanine symporter family protein	50.0	9.6	154.2	3	3	3	8.8
Bhyoa7455_2653	hypothetical protein	45.7	4.4	538.4	13	11	5	29.0
Bhyoa7455_2657	ankyrin repeat-containing protein	27.0	4.0	214.6	4	4	3	21.2
Bhyoa7455_2665	basic membrane lipoprotein	23.2	7.5	404.5	7	6	3	54.4
Bhyoa7455_2671	periplasmic-iron-binding protein BitA	14.8	5.1	133.8	4	3		38.3
Bhyoa7455_2678	**variable surface protein - VspA**	**22.3**	**6.2**	**91.7**	**2**	**2**	**2**	**9.0**
Bhyoa7455_2687	hypothetical protein	15.2	5.6	218.4	4	2		35.6
Bhyoa7455_2691	periplasmic-iron-binding protein BitC	12.8	7.1	311.0	6	5	4	35.7
Bhyoa7455_2694	variable surface protein - VspF	10.9	7.8	826.4	11	9	9	55.8

Proteins in total predicted	271
Lipoproteins predicted by SpLiP	74
beta-barrel proteins predicted by BOMP	32

Proteins detected under iron-restricted conditions in B. hyodysenteriae P8544

Accession	Protein	MW [kDa]	pI	Scores		Peptides		SC
Bhyov8544_0054	PilZ domain containing protein	28.9	5.1	122.4	3	2		17.1
Bhyov8544_0070	hypothetical protein	24.7	4.8	228.0	5	4	3	28.9
Bhyov8544_0095	rplJ 50S ribosomal protein L10	19.2	5.9	197.7	3	3	2	16.4
Bhyov8544_0107	**flaA putative flagellar filament outer layer protein FlaA**	**27.6**	**4.6**	**354.9**	**7**	**5**		**37.3**
Bhyov8544_0108	flaA flagellar filament outer layer protein FlaA	24.7	4.6	238.4	6	5	5	20.4
Bhyov8544_0129	**hypothetical protein**	**38.4**	**8.8**	**121.8**	**4**	**2**		**13.5**
Bhyov8544_0132	**hypothetical protein**	**29.3**	**8.6**	**76.3**	**2**	**2**		**7.0**
Bhyov8544_0143	potD spermidine/putrescine transport ATP-binding protein PotA	45.3	4.6	915.1	19	18	10	37.0

Bhyov8544_0144	ushA putative UshA protein; putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	57.2	4.8	351.2	9	8	4	25.8
Bhyov8544_0150	vspH variable surface protein VspH	47.0	4.9	246.7	5	3		20.9
Bhyov8544_0158	cstA carbon starvation protein CstA	58.6	9.7	164.8	3	2	2	8.1
Bhyov8544_0164	**TRAP transporter solute receptor, TAXI family**	**34.4**	**4.5**	**972.0**	**16**	**15**	**15**	**43.7**
Bhyov8544_0191	hypothetical protein	15.1	9.3	353.2	6	5	2	51.5
Bhyov8544_0192	ptsN phosphotransferase system mannitol/fructose-specific IIA domain	31.2	5.4	246.1	5	5	3	23.2
Bhyov8544_0195	metal dependent amidohydrolase	63.9	5.0	352.3	7	4	4	17.3
Bhyov8544_0205	arp ankyrin repeat-containing protein	15.2	5.4	440.4	8	8	6	60.6
Bhyov8544_0209	hypothetical protein	24.2	4.7	89.3	3	2	2	19.1
Bhyov8544_0219	hypothetical protein	30.5	6.3	395.1	7	5	4	40.5
Bhyov8544_0230	hypothetical protein	20.3	4.4	458.0	10	9	4	34.1
Bhyov8544_0232	periplasmic ATP/GTP-binding protein	32.7	4.3	297.1	5	5	5	31.3
Bhyov8544_0254	nox DH oxidase	50.1	6.1	1093.1	23	17	12	48.9
Bhyov8544_0260	rplY 50S ribosomal protein L25/general stress protein Ctc	21.9	5.6	142.3	4	2	2	29.1
Bhyov8544_0270	**hypothetical protein**	**41.0**	**5.1**	**120.3**	**4**	**3**	**2**	**15.7**
Bhyov8544_0293	binding-protein-dependent transport system, membrane component	35.5	9.8	201.0	4	4	3	15.0
Bhyov8544_0298	**oppA OppA, ABC-type oligopeptide transport system, periplasmic component**	**60.8**	**4.9**	**958.1**	**19**	**17**	**17**	**43.3**
Bhyov8544_0305	putative dynein heavy chain	42.3	4.5	686.7	13	13	11	43.8
Bhyov8544_0315	aminodeoxychorismate lyase	38.1	9.2	303.9	7	6	4	30.1
Bhyov8544_0317	PSP1	37.6	5.0	53.9	3	3	2	5.2
Bhyov8544_0325	hypothetical protein	20.9	4.8	280.9	6	4	4	36.4
Bhyov8544_0354	arp ankyrin repeat-containing protein	71.0	4.6	629.9	12	6	5	23.4
Bhyov8544_0355	solute binding protein-like protein	97.5	4.8	986.5	19	18	19	25.9
Bhyov8544_0364	ABC-type uncharacterized transport system, periplasmic component	32.9	4.4	891.4	16	15		67.3
Bhyov8544_0366	**hypothetical protein**	**18.5**	**4.7**	**170.4**	**3**	**2**		**20.0**
Bhyov8544_0378	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit	48.2	9.9	154.4	4	3	3	12.0

Bhyov8544_0379	biotin/lipoyl attachment domain-containing protein	64.2	5.7	1765.1	34	32	28	64.2
Bhyov8544_0380	hypothetical protein	7.0	9.9	70.8	3	3	2	33.3
Bhyov8544_0417	**hypothetical protein**	**51.3**	**4.8**	**150.5**	**2**	**2**	**2**	**5.2**
Bhyov8544_0435	tauA ABC-type nitrate/sulfonate/bicarbonate transport system	34.1	4.5	746.3	14	14	11	58.3
Bhyov8544_0445	hypothetical protein	19.7	5.5	145.1	2	2		14.0
Bhyov8544_0456	hypothetical protein	24.5	9.2	190.7	4	2		18.0
Bhyov8544_0479	**hypothetical protein**	**56.9**	**4.1**	**171.8**	**5**	**4**	**3**	**11.1**
Bhyov8544_0480	**hypothetical protein**	**37.0**	**4.1**	**341.9**	**6**	**5**	**5**	**17.4**
Bhyov8544_0484	nagE pts system, N-acetylglucosamine-specific iibc component	50.6	8.7	466.6	10	7	6	22.4
Bhyov8544_0496	hypothetical protein	73.8	5.2	666.6	15	11	10	27.7
Bhyov8544_0521	putative positive regulator of sigma E, RseC/MucC	15.8	9.3	294.1	7	5	4	45.7
Bhyov8544_0523	TPR domain-containing protein	53.6	6.0	1144.7	21	17	17	45.2
Bhyov8544_0525	**hypothetical protein**	**40.0**	**5.6**	**123.3**	**3**	**3**	**2**	**13.7**
Bhyov8544_0526	hypothetical protein	38.1	4.8	973.6	22	16	16	51.7
Bhyov8544_0531	dnaJ chaperone protein dnaJ	40.9	9.6	101.1	3	3		11.4
Bhyov8544_0562	fadD acyl-CoA synthetase	62.2	6.6	539.4	11	10	6	29.6
Bhyov8544_0570	TPR domain-containing protein	20.2	4.7	217.3	5	4	4	31.5
Bhyov8544_0584	eno Phosphopyruvate hydratase	47.0	4.8	515.4	11	10	5	35.3
Bhyov8544_0598	amino acid-binding protein	28.6	4.9	614.7	10	9	7	40.6
Bhyov8544_0605	etfB electron transfer flavoprotein beta subunit	28.6	5.8	222.3	5	2	2	28.4
Bhyov8544_0606	acaD acyl-CoA dehydrogenase	40.0	6.1	356.6	7	4		21.8
Bhyov8544_0612	putative V-type ATP synthase subunit I	68.7	6.1	815.7	19	11	10	31.8
Bhyov8544_0622	hypothetical protein	43.1	5.1	318.3	7	5	5	24.7
Bhyov8544_0630	porG pyruvate oxireductase	38.0	9.4	324.7	6	4		20.0
Bhyov8544_0631	porA pyruvate ferredoxin oxireductase	82.9	6.2	283.7	7	4		13.8
Bhyov8544_0643	hypothetical protein	23.5	5.4	236.8	5	4	4	31.9
Bhyov8544_0701	hypothetical protein	41.9	5.3	107.9	5	3		14.0
Bhyov8544_0728	ftsY Signal recognition particle GTPase	35.4	9.1	849.8	13	12	9	42.1
Bhyov8544_0780	hypothetical protein	37.9	4.6	161.9	5	6	4	18.1

Bhyov8544_0782	extracellular solute-binding protein, family 5	59.7	4.6	1275.0	26	22	20	46.8
Bhyov8544_0798	hypothetical protein	33.4	5.0	468.4	9	6	5	34.2
Bhyov8544_0804	thrS threonyl-tRNA synthetase	73.9	5.8	314.3	7	5	5	16.5
Bhyov8544_0816	cheW purine-binding chemotaxis protein	17.9	4.3	123.3	2	3		23.9
Bhyov8544_0832	rsgA non-heme iron-containing ferritin	20.8	4.9	142.8	5	4		28.9
Bhyov8544_0837	pep peptidase	47.1	5.3	117.6	4	4	3	7.1
Bhyov8544_0875	hypothetical protein	35.6	4.8	1604.5	30	29	28	80.9
Bhyov8544_0876	hypothetical protein	16.9	0.0	97.0	3	2		11.5
Bhyov8544_0895	OmpA family protein	25.2	9.6	195.6	4	3		16.3
Bhyov8544_0896	hypothetical protein	26.2	9.3	273.0	6	5	4	32.2
Bhyov8544_0902	fusA elongation factor G	75.3	5.1	491.6	13	10	7	26.5
Bhyov8544_0903	tufA elongation factor Tu	44.4	5.8	765.2	14	14	11	47.3
Bhyov8544_0917	rplE 50S ribosomal protein L5	21.1	10.1	267.8	6	4	3	33.2
Bhyov8544_0918	rpsH 30S ribosomal protein S8	14.9	9.7	193.4	4	3	2	38.3
Bhyov8544_0953	hypothetical protein	14.8	4.8	157.0	4	4		42.5
Bhyov8544_0955	**hypothetical protein**	**36.1**	**6.1**	**163.1**	**4**	**2**		**15.7**
Bhyov8544_0996	gltP GltP, Na+/H+-dicarboxylate symporter	40.2	9.2	124.3	3	2	2	13.0
Bhyov8544_1024	phoB alkaline phosphatase III	57.7	4.8	1471.2	24	18	17	58.3
Bhyov8544_1046	flaA flagellar filament outer layer protein FlaA	36.0	4.7	637.8	11	7	5	40.6
Bhyov8544_1057	Bhyov8544_1057 hypothetical protein	51.2	8.8	698.7	12	11	6	26.2
Bhyov8544_1080	vspF variable surface protein - VspF	3.6	4.1	168.9	5	5	4	71.9
Bhyov8544_1087	hypothetical protein	18.8	5.2	507.8	10	9	8	56.7
Bhyov8544_1090	hypothetical protein	37.2	4.9	113.3	4	3	3	11.3
Bhyov8544_1099	hypothetical protein	15.3	4.3	369.3	8	5	3	51.2
Bhyov8544_1121	hypothetical protein	38.6	4.4	150.8	4	4		19.3
Bhyov8544_1130	integral membrane transport protein	47.7	8.8	198.7	5	5	4	14.7
Bhyov8544_1150	rnfC electron transport complex protein 1	46.8	8.6	1631.4	30	29	25	60.5
Bhyov8544_1152	rnfG putative electron transport complex	19.9	4.5	850.9	16	12	9	58.6
Bhyov8544_1168	hypothetical protein	39.3	5.0	170.8	4	4	4	13.2
Bhyov8544_1201	hypothetical protein	22.0	9.1	294.1	5	4	3	25.9

Bhyov8544_1215	hypothetical protein	40.0	4.4	857.6	15	14	13	35.3
Bhyov8544_1218	hypothetical protein	19.7	5.7	76.8	2	2		5.6
Bhyov8544_1233	fabF 3-oxoacyl-ACP (acyl carrier protein) synthase II	44.5	6.1	87.9	3	2		11.5
Bhyov8544_1240	secG putative preprotein translocase subunit SecG	12.3	9.4	109.7	2	2		14.3
Bhyov8544_1247	**AMP-activated protein kinase (AMPK) beta subunit glycogen binding domain (GBD)**	**29.4**	**4.8**	**138.9**	**4**	**3**	**2**	**26.1**
Bhyov8544_1254	hslJ Heat shock protein	17.2	4.1	572.0	9	7	6	37.4
Bhyov8544_1297	extracellular solute-binding protein, family 5	60.8	5.1	613.1	13	10	9	27.9
Bhyov8544_1298	extracellular solute-binding protein, family 5	60.7	4.7	529.9	12	9	9	35.9
Bhyov8544_1303	hypothetical protein	16.5	9.6	127.9	3	3	2	28.5
Bhyov8544_1311	tpx peroxiredoxin family, thiol peroxidase	17.9	5.2	575.1	9	8	8	70.9
Bhyov8544_1329	thiol-disulfide interchange protein DsbD-like protein	31.6	5.4	487.0	11	8	5	45.8
Bhyov8544_1330	thiol-disulfide interchange protein DsbD-like protein	31.2	4.6	164.0	4	3	2	19.6
Bhyov8544_1347	hypothetical protein	44.7	7.5	498.1	10	6	3	36.1
Bhyov8544_1352	TPR domain-containing protein	27.2	9.3	197.2	4	3	2	21.1
Bhyov8544_1373	bitB periplasmic-iron-binding protein BitB	38.2	4.7	319.2	6	4	3	18.3
Bhyov8544_1377	extracellular solute-binding protein, family 3	30.1	5.3	956.4	16	14	14	58.7
Bhyov8544_1389	mglB galactose/glucose-binding protein	37.8	4.4	837.7	15	11	7	52.9
Bhyov8544_1390	mglB galactose/glucose-binding protein	38.2	4.7	2604.5	45	44	37	74.9
Bhyov8544_1411	ushA UshA, 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	68.3	4.7	748.9	13	6	6	27.0
Bhyov8544_1438	flavodoxin	18.8	8.8	61.4	2	2		12.2
Bhyov8544_1477	ahpC alkyl hydrogen peroxide reductase	20.9	5.3	158.7	4	4	2	31.0
Bhyov8544_1489	ABC transporter, transmembrane region	73.3	9.3	105.4	2	2	2	6.3
Bhyov8544_1500	groEL chaperonin GroEL	58.2	4.9	1009.0	19	15	12	44.6
Bhyov8544_1510	hypothetical protein	26.2	4.9	255.8	5	4	2	23.9
Bhyov8544_1522	putative Na+/phosphate symporter	61.9	6.3	280.9	6	4	3	16.4
Bhyov8544_1528	non-heme iron-containing ferritin	20.0	5.0	380.6	9	8	8	55.0
Bhyov8544_1587	faa1 Long-chain acyl-CoA synthetases (AMP-forming)	71.2	7.7	210.3	5	4	4	14.1
Bhyov8544_1600	biopolymer transport protein ExbB	22.5	5.0	133.1	4	4	2	23.3
Bhyov8544_1626	gldG ABC-type uncharacterized transport system	61.4	9.4	459.1	10	6	6	25.1
Bhyov8544_1635	tar8 putative methyl-accepting chemotaxis protein	74.0	4.4	288.5	8	5	3	13.4

Bhyov8544_1637	cheY chemotaxis response regulator CheY	13.5	7.6	257.1	6	4	2	68.0
Bhyov8544_1642	cheB response regulator receiver modulated CheB methylesterase	41.0	9.0	237.5	4	3		21.2
Bhyov8544_1645	putative transcriptional regulator	40.5	9.5	125.8	4	3		12.7
Bhyov8544_1649	undefined product	47.0	9.6	103.9	2	2		5.1
Bhyov8544_1661	lmp1 TPR domain-containing protein	52.5	5.1	956.4	21	19	12	47.9
Bhyov8544_1663	rpsB 30S ribosomal protein S2	29.6	5.0	199.1	5	5	4	27.8
Bhyov8544_1670	oppA ABC-type oligopeptide transport system, periplasmic component	60.7	4.7	1173.9	24	22	19	40.6
Bhyov8544_1696	bmpB BmpB, outer membrane lipoprotein	29.7	4.3	688.9	12	10	10	36.9
Bhyov8544_1705	hypothetical protein	19.3	5.2	577.0	12	10	9	65.5
Bhyov8544_1715	Predicted membrane protein	23.2	10.6	124.0	2	2		11.6
Bhyov8544_1732	**hypothetical protein**	**60.6**	**5.9**	**874.9**	**18**	**16**	**14**	**39.9**
Bhyov8544_1738	hypothetical protein	27.5	5.0	180.3	3	2	2	13.5
Bhyov8544_1764	mreB rod shape-determining protein mreB	35.9	5.5	232.0	4	3	2	24.6
Bhyov8544_1779	hppA membrane-bound proton-translocating pyrophosphatase	79.9	5.9	762.6	13	12	11	16.3
Bhyov8544_1799	outer membrane protein	100.3	6.7	889.7	16	15	13	22.6
Bhyov8544_1823	**arp ankyrin repeat-containing protein**	**87.9**	**4.6**	**258.2**	**5**	**4**		**9.8**
Bhyov8544_1866	rsxE SoxR-reducing system protein RsxE	23.4	10.0	139.4	2	2	2	5.0
Bhyov8544_1867	rnfA RnfA, Predicted DH:ubiquinone oxidoreductase, subunit RnfA	21.1	9.4	107.2	2	2	2	5.7
Bhyov8544_1868	ferredoxin	29.6	9.4	615.1	12	12	7	44.3
Bhyov8544_1900	**hypothetical protein**	**65.2**	**4.2**	**175.4**	**4**	**4**	**2**	**7.2**
Bhyov8544_1921	basic membrane lipoprotein	38.6	4.6	242.0	6	2		31.1
Bhyov8544_1922	**basic membrane lipoprotein**	**36.9**	**4.6**	**985.4**	**19**	**16**	**14**	**53.5**
Bhyov8544_1931	hypothetical protein	10.0	5.4	310.1	8	6	6	54.5
Bhyov8544_1933	hypothetical protein	41.2	5.0	424.9	9	7	2	25.0
Bhyov8544_1938	extracellular solute-binding protein, family 3	29.2	4.5	1873.4	26	24	24	52.5
Bhyov8544_1944	lea hypothetical protein	18.4	9.3	495.8	9	9	8	58.3
Bhyov8544_1966	spoIIAA SpoIIAA, Anti-anti-sigma regulatory factor	12.2	5.2	87.3	2	2	2	26.4

Bhyov8544_1973	**vspE variable surface protein - VspE**	**40.5**	**6.5**	**422.9**	**7**	**5**	**4**	**27.7**
Bhyov8544_1987	hypothetical protein	11.8	6.1	156.2	4	4	3	44.8
Bhyov8544_2002	**hypothetical protein**	**15.5**	**9.5**	**152.3**	**2**	**2**	**2**	**18.6**
Bhyov8544_2009	ompA outer membrane protein	22.6	9.4	236.8	6	6	6	41.4
Bhyov8544_2010	ompA OmpA family protein	23.9	4.6	436.7	8	8	6	59.6
Bhyov8544_2034	motB putative flagellar motor protein	28.9	7.5	334.4	6	5	4	33.8
Bhyov8544_2035	motA Flagellar Motor Protein	27.8	4.8	585.3	9	8	7	34.2
Bhyov8544_2044	extracellular solute-binding protein, family 5 2	61.8	4.9	2791.6	54	51	44	61.3
Bhyov8544_2064	hypothetical protein	28.1	4.6	497.3	10	7	4	46.1
Bhyov8544_2069	flaB3 periplasmic flagellar filament protein FlaB3	30.1	5.2	869.7	16	7	7	54.0
Bhyov8544_2071	Zn dependant metalloprotease	25.8	9.1	207.6	4	4	3	17.8
Bhyov8544_2075	hypothetical protein	60.5	8.4	386.2	8	8	6	20.4
Bhyov8544_2078	argH argininosuccinate lyase	45.6	5.6	369.5	9	4	4	27.3
Bhyov8544_2088	flaB Flagellar filament core protein flaB2	28.2	5.4	487.2	10	9	4	38.6
Bhyov8544_2097	**hypothetical protein**	**143.4**	**6.7**	**691.5**	**15**	**11**		**12.7**
Bhyov8544_2111	nifS NifS, Cysteine sulfinate desulfinase/cysteine desulfurase-like enzyme	42.9	6.1	441.5	10	5	4	37.1
Bhyov8544_2129	hypothetical protein	26.8	5.0	1318.7	23	21	20	58.5
Bhyov8544_2147	**arp ankyrin repeat-containing protein**	**61.1**	**4.3**	**1428.9**	**24**	**17**	**16**	**47.8**
Bhyov8544_2151	hypothetical protein	15.1	4.5	181.1	3	3		27.6
Bhyov8544_2152	**hypothetical protein**	**59.3**	**4.8**	**525.9**	**12**	**11**	**9**	**24.7**
Bhyov8544_2171	periplasmic solute binding protein	32.3	4.6	356.9	7	5	4	30.3
Bhyov8544_2173	**vspA variable surface protein A**	**38.1**	**4.5**	**606.9**	**10**	**5**	**3**	**37.9**
Bhyov8544_2176	ABC transporter substrate binding protein	35.1	4.6	1055.3	16	15	11	55.9
Bhyov8544_2184	hypothetical protein	30.7	4.5	856.8	18	18	17	54.6
Bhyov8544_2185	**hypothetical protein**	**58.0**	**4.9**	**810.8**	**13**	**13**	**11**	**23.1**
Bhyov8544_2186	**hypothetical protein**	**59.1**	**4.8**	**329.9**	**7**	**6**	**5**	**14.3**

Bhyov8544_2190	secA preprotein translocase, SecA subunit	111.0	5.9	613.2	12	11	9	18.5
Bhyov8544_2193	bitC periplasmic-iron-binding protein BitC	8.4	7.1	132.7	3	2		56.8
Bhyov8544_2195	outer membrane protein	52.7	4.7	136.9	3	3		7.3
Bhyov8544_2196	mtrC membrane fusion protein	45.0	7.2	424.3	9	6	3	26.5
Bhyov8544_2199	hypothetical protein	23.3	6.4	546.0	8	7	6	38.3
Bhyov8544_2209	hypothetical protein	25.1	4.5	397.9	9	7	4	33.2
Bhyov8544_2217	oppA oligopeptide ABC transporter periplasmic subunit	61.3	5.9	702.8	14	12	7	27.6
Bhyov8544_2228	arp ankyrin repeat-containing protein	43.3	4.6	269.1	8	7	6	23.3
Bhyov8544_2264	undefined product	16.8	9.9	320.2	6	3	2	44.0
Bhyov8544_2284	Rieske (2Fe-2S) domain protein	38.0	9.7	280.4	11	10	8	8.0
Bhyov8544_2321	basic membrane lipoprotein	17.9	4.2	222.2	5	4	3	40.4
Bhyov8544_2345	extracellular solute-binding protein, family 5	60.3	4.7	831.2	16	13	19	37.8
Bhyov8544_2346	extracellular solute-binding protein, family 6	59.4	4.8	1414.5	24	22	18	47.0
Bhyov8544_2347	extracellular solute-binding protein, family 7	62.3	5.0	914.8	17	17	15	40.2
Bhyov8544_2372	glyceraldehyde-3-phosphate dehydrogenase	38.1	7.8	593.9	11	10	9	41.2
Bhyov8544_2373	pgk phosphoglycerate kinase	44.1	5.8	295.2	5	3	3	23.6
Bhyov8544_2385	hypothetical protein	53.9	5.1	368.5	8	4	4	24.8
Bhyov8544_2387	hypothetical protein	50.0	5.0	227.7	6	3	3	18.7
Bhyov8544_2403	arp ankyrin repeat-containing protein	40.7	4.3	744.0	16	12	9	40.7
Bhyov8544_2407	cutF lipoprotein involved with copper homeostasis and adhesion	14.7	4.0	260.1	4	4	3	26.0
Bhyov8544_2410	msrAB bifunctional methionine sulfoxide reductase	23.3	6.6	165.7	5	4	3	51.0
Bhyov8544_2417	**hypothetical protein**	**28.2**	**5.5**	**268.8**	**5**	**5**	**4**	**22.8**
Bhyov8544_2426	phosphoenolpyruvate carboxykinase (GTP)	66.7	5.8	175.0	6	5		9.5
Bhyov8544_2437	extracellular solute-binding protein, family 3	30.4	4.7	1148.6	19	19	18	53.8
Bhyov8544_2438	extracellular solute-binding protein, family 4	31.1	4.8	1065.4	16	15	14	60.7
Bhyov8544_2442	endoribonuclease	13.9	5.3	166.4	3	2	2	22.0
Bhyov8544_2464	ptsG fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB , and IIA components	77.4	6.1	521.3	12	8	5	27.5
Bhyov8544_2465	tar methyl-accepting chemotaxis protein	63.7	4.7	132.2	3	2	2	6.3
Bhyov8544_2471	rbr rubrerythrin	20.6	5.9	517.2	8	7	7	44.4
Bhyov8544_2472	sodA superoxide dismutase	22.1	6.3	70.5	4	3		23.2

Bhyov8544_2483	undefined product	53.4	5.4	91.2	4	3		7.1
Bhyov8544_2503	hypothetical protein	18.8	7.2	363.4	6	6		33.5
Bhyov8544_2504	hypothetical protein	18.5	7.2	351.5	6	6	3	32.7
Bhyov8544_2511	iron-containing alcohol dehydrogenase	42.0	5.5	335.3	7	5		22.0
Bhyov8544_2549	fliL putative flagellar basal body-associated protein	20.2	4.6	918.2	15	15	14	60.2
Bhyov8544_2559	secF preprotein translocase	34.3	8.8	329.5	4	4	4	20.8
Bhyov8544_2560	secD preprotein translocase subunit SecD	55.1	5.0	1111.3	18	17	13	33.6
Bhyov8544_2561	yajC putative preprotein translocase subunit	15.8	9.5	540.2	8	6	6	38.5
Bhyov8544_2610	oppA ABC-type oligopeptide transport system, periplasmic component	59.8	5.1	1778.3	33	29	24	56.5
Bhyov8544_2611	oppA ABC-type oligopeptide transport system, periplasmic component	61.2	5.4	149.5	3	3		8.4
Bhyov8544_2645	feoB ferrous iron transport protein B	92.3	6.1	1652.0	30	28	25	32.9
Bhyov8544_2648	hypothetical protein	50.0	4.7	525.7	9	9	7	20.6
Bhyov8544_2659	hypothetical protein	14.9	4.5	320.5	6	4	3	22.9
Bhyov8544_2667	**putative inversin protein alternative isoform**	**64.3**	**4.2**	**420.4**	**8**	**7**	**7**	**21.0**
Bhyov8544_2672	bitB periplasmic-iron-binding protein BitB	35.6	4.8	392.7	8	8	6	40.7
Bhyov8544_2693	**basic membrane lipoprotein**	**23.2**	**7.5**	**74.2**	**2**	**2**		**12.0**
Bhyov8544_2696	bitC periplasmic-iron-binding protein BitC	24.3	4.8	210.8	4	4	4	23.5
Bhyov8544_2713	vspF variable surface protein	14.1	9.6	1211.0	22	20	20	77.3
Bhyov8544_2731	**bitB periplasmic-iron-binding protein BitB**	**10.0**	**9.0**	**235.3**	**5**	**5**	**3**	**75.3**

Predicted proteins under iron-restricted conditions in B. hyodysenteriae P7455

Accession	Protein	MW [kDa]	pI	Scores		Peptides		SC
Bhyoa7455_0028	methyl-accepting chemotaxis protein McpB	84.5	6.0	216.9	5	5	4	9.4
Bhyoa7455_0035	acetylglutamate kinase	31.1	5.1	86.2	5	4		14.9

Bhyoa7455_0038	biopolymer transport protein ExbB	22.5	5.0	163.3	4	2		23.8
Bhyoa7455_0055	ABC-type oligopeptide transport system, periplasmic component	60.7	4.7	1625.4	28	21	22	43.1
Bhyoa7455_0062	30S ribosomal protein S2	29.6	5.0	328.5	7	6		42.1
Bhyoa7455_0064	TPR domain-containing protein	52.5	5.1	621.5	13	12	3	39.1
Bhyoa7455_0115	putative dynein heavy chain	42.4	4.5	795.5	14	10	13	42.5
Bhyoa7455_0127	aminodeoxychorismate lyase	38.1	9.2	87.1	2	2		14.3
Bhyoa7455_0129	PSP1	37.6	5.0	104.0	5	3	2	7.0
Bhyoa7455_0137	hypothetical protein	20.9	4.8	229.6	6	5	4	38.1
Bhyoa7455_0174	phosphate ABC transporter, phosphate-binding protein	27.5	4.3	359.0	6	3		40.2
Bhyoa7455_0180	ABC-type uncharacterized transport system, periplasmic component	32.9	4.4	744.8	14	13	9	83.0
Bhyoa7455_0181	**hypothetical protein**	**19.8**	**5.8**	**216.4**	**6**	**3**		**56.6**
Bhyoa7455_0182	hypothetical protein	18.6	4.7	265.7	5	4	3	25.5
Bhyoa7455_0185	hypothetical protein	68.5	6.4	68.8	4	3		10.4
Bhyoa7455_0195	biotin/lipoyl attachment domain-containing protein	64.2	5.7	1859.1	36	28	24	64.7
Bhyoa7455_0250	ABC-type nitrate/sulfonate/bicarbonate transport system	37.2	4.5	834.1	14	13	9	46.1
Bhyoa7455_0260	hypothetical protein	19.7	5.5	124.5	2	2		14.0
Bhyoa7455_0271	hypothetical protein	24.5	9.2	196.8	3	3	2	16.7
Bhyoa7455_0294	**hypothetical protein**	**57.0**	**4.1**	**100.9**	**2**	**2**		**5.0**
Bhyoa7455_0295	**hypothetical protein**	**38.2**	**4.1**	**320.1**	**5**	**4**	**3**	**19.6**
Bhyoa7455_0299	pts system, N-acetylglucosamine-specific iibc component	50.6	8.7	599.5	12	9	8	28.5
Bhyoa7455_0311	**hypothetical protein**	**73.8**	**5.1**	**175.5**	**4**	**2**	**2**	**8.5**
Bhyoa7455_0336	putative positive regulator of sigma E, RseC/MucC	15.8	9.3	147.8	4	4	3	23.6
Bhyoa7455_0338	TPR domain-containing protein	53.6	6.0	916.2	18	15	9	39.2
Bhyoa7455_0340	hypothetical protein	40.0	5.6	179.7	4	4		17.1
Bhyoa7455_0341	**hypothetical protein**	**38.1**	**4.8**	**905.6**	**22**	**16**	**11**	**44.1**
B.yoa7455_0367	galactose/glucose-binding protein	38.2	4.7	4325.2	74	61	57	78.9
Bhyoa7455_0368	galactose/methyl galaxtoside transporter ATP-binding protein	56.1	9.1	326.2	7	4	3	16.0
Bhyoa7455_038	**OppA, ABC-type oligopeptide transport system, periplasmic**	**60.8**	**4.9**	**912.6**	**17**	**15**	**13**	**41.8**

2	**component**							
Bhyoa7455_0387	binding-protein-dependent transport system, membrane component	35.5	9.8	162.7	4	3	3	15.3
Bhyoa7455_0404	OppA, ABC-type oligopeptide transport system, periplasmic component	59.4	4.6	293.3	7	7	5	14.2
Bhyoa7455_0418	50S ribosomal protein L25/general stress protein Ctc	21.9	5.6	162.0	4	4		27.6
Bhyoa7455_0424	DH oxidase	50.1	6.1	803.9	14	14	7	41.6
Bhyoa7455_0442	**hypothetical protein**	**41.7**	**4.6**	**199.6**	**3**	**3**		**12.9**
Bhyoa7455_0446	periplasmic ATP/GTP-binding protein	32.7	4.3	294.9	5	4		26.5
Bhyoa7455_0448	hypothetical protein	20.3	4.4	227.0	5	4	3	30.6
Bhyoa7455_0459	hypothetical protein	30.5	6.0	252.3	5	5	3	26.4
Bhyoa7455_0469	hypothetical protein	24.2	4.7	368.4	6	5	5	43.9
Bhyoa7455_0473	ankyrin repeat-containing protein	15.2	5.4	227.9	5	4	2	52.6
Bhyoa7455_0483	metal dependent amidohydrolase	63.9	5.0	654.0	9	9	6	23.9
Bhyoa7455_0487	hypothetical protein	15.2	0.0	281.9	4	4	4	36.0
Bhyoa7455_0517	TRAP transporter solute receptor, TAXI family	34.4	4.5	810.3	16	15	12	54.4
Bhyoa7455_0523	carbon starvation protein CstA	58.6	9.7	369.4	7	5	3	16.7
Bhyoa7455_0531	variable surface protein VspH	47.0	4.9	1019.2	15	14	10	47.0
Bhyoa7455_0537	putative UshA protein; putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	57.2	4.8	910.8	17	10	12	48.6
Bhyoa7455_0538	spermidine/putrescine transport ATP-binding protein PotA	45.3	4.6	501.9	9	8	4	32.8
Bhyoa7455_0549	**hypothetical protein**	**29.3**	**8.6**	**131.7**	**3**	**3**	**2**	**13.6**
Bhyoa7455_0550	hypothetical protein	27.5	9.6	158.7	5	3	5	18.3
Bhyoa7455_0573	flagellar filament outer layer protein FlaA	24.7	4.6	880.9	16	10	6	65.7
Bhyoa7455_0574	**putative flagellar filament outer layer protein FlaA**	**27.6**	**4.6**	**604.8**	**11**	**10**	**9**	**53.1**
Bhyoa7455_0586	50S ribosomal protein L10	19.2	5.9	232.5	5	3	3	39.0
Bhyoa7455_0604	putative peptidoglycan-binding LysM:Peptidase M23B family	67.7	9.4	138.5	4	4		10.2
Bhyoa7455_0612	hypothetical protein	24.7	4.8	263.2	5	3	3	31.2
Bhyoa7455_0685	putative flavoprotein	45.8	5.5	164.6	4	4		18.3
Bhyoa7455_0691	outer membrane protein	100.3	6.7	548.0	10	8	5	15.1
Bhyoa7455_0711	membrane-bound proton-translocating pyrophosphatase	79.8	5.9	465.1	8	8	7	13.3

Bhyoa7455_0792	alkaline phosphatase III	57.7	4.8	1424.7	23	17	16	53.2
Bhyoa7455_0814	flagellar filament outer layer protein FlaA	36.0	4.7	796.8	13	13	8	45.9
Bhyoa7455_0825	hypothetical protein	51.2	8.8	681.9	11	8	6	28.8
Bhyoa7455_0856	**UshA, 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase**	**68.3**	**4.7**	**845.6**	**15**	**11**	**6**	**39.6**
Bhyoa7455_0941	peptidase	47.1	5.3	109.5	3	3		7.1
Bhyoa7455_0946	non-heme iron-containing ferritin	20.9	4.9	221.9	5	6		28.9
Bhyoa7455_0980	hypothetical protein	33.4	5.0	132.4	3	3	3	17.1
Bhyoa7455_0997	alkyl hydrogen peroxide reductase	20.9	5.3	366.7	9	8	6	49.7
Bhyoa7455_1004	extracellular solute-binding protein, family 5	61.7	4.8	237.8	5	4	5	11.1
Bhyoa7455_1020	chaperonin GroEL	58.2	4.9	261.5	6	3		19.7
Bhyoa7455_1029	**hypothetical protein**	**22.2**	**5.2**	**165.6**	**2**	**2**	**2**	**15.4**
Bhyoa7455_1048	non-heme iron-containing ferritin	20.0	5.0	679.6	13	11	8	69.6
Bhyoa7455_1049	methyl-accepting chemotaxis protein McpB	68.3	4.7	174.6	3	2		7.0
Bhyoa7455_1071	3-hydroxybutyryl-CoA dehydratase	29.9	8.8	287.1	5	3		34.3
Bhyoa7455_1072	3-hydroxybutyryl-CoA dehydratase	27.7	5.4	673.9	10	11	4	48.1
B.hyoa7455_1073	acetyl-CoA acetyltransferase	40.9	8.8	468.0	9	7	5	30.1
Bhyoa7455_1098	**acetyltransferase, GT family**	**20.9**	**5.2**	**133.3**	**3**	**2**		**5.7**
Bhyoa7455_1102	glucose-1-phosphate adenylyltransferase	48.2	8.5	270.9	7	6		26.4
Bhyoa7455_1135	flagellar protein	28.8	5.5	792.8	14	12	8	51.5
Bhyoa7455_1150	peroxiredoxin family, thiol peroxidase	17.9	5.2	561.5	10	10	8	70.9
Bhyoa7455_1153	chemotaxis response regulator CheY	16.0	9.3	51.8	2	2		22.7
Bhyoa7455_1158	hypothetical protein	22.0	9.5	157.8	4	4	4	26.0
Bhyoa7455_1164	extracellular solute-binding protein, family 5	60.8	5.2	879.5	23	12	14	47.0
Bhyoa7455_1180	hypothetical protein	38.1	10.6	184.0	3	3	3	10.2
Bhyoa7455_1183	**hypothetical protein**	**33.5**	**4.9**	**150.2**	**3**	**3**		**16.1**
Bhyoa7455_1206	Heat shock protein	17.2	4.1	282.8	6	6	6	28.2
Bhyoa7455_1239	Signal recognition particle GTPase	35.4	9.1	808.8	12	11	7	39.0
Bhyoa7455_1252	NifS, Cysteine sulfinate desulfinase/cysteine desulfurase-like	42.9	5.9	219.9	7	5	3	26.5

	enzyme							
Bhyoa7455_1272	hypothetical protein	26.8	4.9	1239.4	20	18	7	58.1
Bhyoa7455_1290	ankyrin repeat-containing protein	61.1	4.3	1421.0	21	18	13	51.3
Bhyoa7455_1308	integral membrane transport protein	46.1	5.4	189.4	5	3	3	17.7
Bhyoa7455_1322	**hypothetical protein**	**44.1**	**5.9**	**80.4**	**3**	**3**		**7.4**
Bhyoa7455_1328	electron transport complex protein	46.8	8.6	1249.5	23	19	11	51.3
Bhyoa7455_1330	putative electron transport complex	19.9	4.5	648.9	11	8	6	54.5
Bhyoa7455_1338	phosphoglycerate kinase	44.1	5.8	264.3	5	5	4	21.7
Bhyoa7455_1339	glyceraldehyde-3-phosphate dehydrogenase	38.1	7.8	780.0	14	12	11	52.4
Bhyoa7455_1359	galactose/glucose-binding protein	37.8	4.4	822.1	13	12	11	48.8
Bhyoa7455_1362	flavodoxin	15.3	4.1	355.1	5	3		74.1
Bhyoa7455_1371	extracellular solute-binding protein, family 3	30.1	5.3	759.1	14	12	11	52.4
Bhyoa7455_1375	periplasmic-iron-binding protein BitB	38.2	4.7	279.7	5	4		24.8
Bhyoa7455_1412	hypothetical protein	63.4	7.5	119.4	5	5		9.0
Bhyoa7455_1416	thiol-disulfide interchange protein DsbD-like protein	31.6	5.4	283.3	6	5		27.3
Bhyoa7455_1427	hypothetical protein	14.9	4.5	188.0	3	3	3	22.9
Bhyoa7455_1437	hypothetical protein	27.5	5.0	206.2	4	3	2	18.7
Bhyoa7455_1443	**hypothetical protein**	**60.7**	**5.9**	**823.7**	**17**	**13**	**8**	**34.8**
Bhyoa7455_1470	hypothetical protein	19.3	5.2	514.9	12	8	6	76.0
Bhyoa7455_1479	BmpB, outer membrane lipoprotein	29.7	4.3	616.0	9	9	6	33.9
Bhyoa7455_1502	acyl-CoA synthetase	62.2	6.6	957.8	16	12	12	39.9
Bhyoa7455_1522	Phosphopyruvate hydratase	47.0	4.8	684.6	11	10	2	47.6
Bhyoa7455_1544	acyl-CoA dehydrogenase	40.0	6.1	391.1	8	8	2	36.8
Bhyoa7455_1547	V-type ATP synthase subunit A	65.1	5.0	195.8	4	3		12.6
Bhyoa7455_1550	putative V-type ATP synthase subunit I	68.7	6.1	560.2	10	9	7	22.5
Bhyoa7455_1583	hypothetical protein	35.6	4.8	1846.4	32	25	24	84.2
Bhyoa7455_1611	elongation factor Tu	44.4	5.8	1032.6	17	17	16	50.2
Bhyoa7455_1625	50S ribosomal protein L5	21.1	10.1	138.2	4	2		21.4
Bhyoa7455_1663	methyl-accepting chemotaxis protein McpB	81.0	5.2	165.9	4	3		8.4

Bhyoa7455_1674	extracellular solute-binding protein, family 5	59.4	4.6	1440.3	26	18	18	52.8
Bhyoa7455_1675	hypothetical protein	11.8	6.1	111.9	4	3		44.8
Bhyoa7455_1684	TPR domain-containing protein	68.3	5.1	223.0	10	4		6.8
Bhyoa7455_1686	**hypothetical protein**	**15.5**	**9.5**	**157.8**	**2**	**2**		**18.6**
Bhyoa7455_1693	OmpA family protein	23.9	4.6	284.6	6	6		45.5
Bhyoa7455_1708	SoxR-reducing system protein RsxE	23.4	10.0	113.8	2	2	2	5.0
Bhyoa7455_1709	RnfA, Predicted DH:ubiquinone oxidoreductase, subunit RnfA	21.1	9.4	115.3	2	2	2	5.7
Bhyoa7455_1735	adenylate kinase	20.7	5.1	100.9	3	3		23.2
Bhyoa7455_1770	**hypothetical protein**	**59.1**	**4.8**	**212.9**	**6**	**5**	**3**	**14.1**
Bhyoa7455_1771	**hypothetical protein**	**58.0**	**4.9**	**383.4**	**7**	**6**	**5**	**17.1**
Bhyoa7455_1772	hypothetical protein	30.7	4.5	524.0	11	10	8	42.1
Bhyoa7455_1780	ABC transporter substrate binding protein	35.1	4.6	995.4	15	13	12	51.1
Bhyoa7455_1783	**variable surface protein A**	**38.1**	**4.5**	**521.2**	**10**	**9**	**7**	**40.8**
Bhyoa7455_1785	periplasmic solute binding protein	32.3	4.6	347.0	6	5	3	33.8
Bhyoa7455_1808	hypothetical protein	27.9	8.7	145.6	4	3	2	19.4
Bhyoa7455_1821	pyruvate oxireductase	38.0	9.4	236.1	7	3		23.2
Bhyoa7455_1832	hypothetical protein	23.5	5.4	304.7	7	5	3	48.4
Bhyoa7455_1864	hypothetical protein	28.0	10.2	90.9	4	3		14.0
Bhyoa7455_1881	Phosphoenolpyruvate-protein phosphotransferase	64.3	4.8	381.8	8	3		18.1
Bhyoa7455_1884	Flagellar Motor Protein	27.8	4.8	301.1	6	5	3	31.6
Bhyoa7455_1893	extracellular solute-binding protein, family 5	61.8	4.9	2932.2	52	40	47	65.0
Bhyoa7455_1913	hypothetical protein	28.1	4.6	334.6	7	6	5	43.8
Bhyoa7455_1918	periplasmic flagellar filament protein FlaB3	30.1	5.2	2120.6	31	32	14	73.4
Bhyoa7455_1920	Zn dependant metalloprotease	25.8	9.1	219.4	4	4	3	20.3
Bhyoa7455_1922	methyl-accepting chemotaxis protein McpA	45.1	5.5	286.9	6	4		18.1
Bhyoa7455_1930	hypothetical protein	39.4	4.9	160.4	5	2	2	16.7
Bhyoa7455_1946	hypothetical protein	28.6	4.9	463.2	6	5	5	25.4
Bhyoa7455_1947	hypothetical protein	27.2	9.2	374.1	8	8	7	19.4

Bhyoa7455_1957	hypothetical protein	40.4	5.7	151.1	3	3		12.7
Bhyoa7455_1969	hypothetical protein	18.8	5.2	502.3	9	7	6	50.3
B.hyoa7455_1981	hypothetical protein	15.3	4.3	140.2	2	2	2	18.9
Bhyoa7455_2025	hypothetical protein	18.8	4.5	147.9	2	2	2	15.5
Bhyoa7455_2046	hypothetical protein	39.9	4.4	952.8	16	13	13	37.1
Bhyoa7455_2064	3-oxoacyl-ACP (acyl carrier protein) synthase II	44.5	6.1	158.7	3	3	3	13.9
Bhyoa7455_2088	methyl-accepting chemotaxis protein McpB	61.3	4.8	103.0	2	2		5.1
Bhyoa7455_2111	ankyrin repeat-containing protein	42.6	4.6	87.5	4	3	2	12.9
Bhyoa7455_2148	-	16.8	9.9	219.7	4	3	2	32.1
Bhyoa7455_2168	Rieske (2Fe-2S) domain protein	38.1	9.7	418.2	15	12	12	10.2
Bhyoa7455_2176	basic membrane lipoprotein	38.6	4.6	586.0	9	8	4	39.7
Bhyoa7455_2177	**basic membrane lipoprotein**	**36.9**	**4.6**	**1012.5**	**17**	**14**	**13**	**55.6**
Bhyoa7455_2185	hypothetical protein	10.0	5.4	281.3	6	5	4	47.7
Bhyoa7455_2192	extracellular solute-binding protein, family 3	29.2	4.5	2189.8	27	27	31	77.4
Bhyoa7455_2198	hypothetical protein	18.4	9.3	643.7	11	10	8	62.0
Bhyoa7455_2210	ankyrin repeat-containing protein	40.4	4.3	407.3	9	7	5	29.5
Bhyoa7455_2214	lipoprotein involved with copper homeostasis and adhesion	14.5	4.0	252.4	3	3	2	26.2
Bhyoa7455_2224	**hypothetical protein**	**28.2**	**5.5**	**195.3**	**4**	**3**	**3**	**22.4**
Bhyoa7455_2234	phosphoenolpyruvate carboxykinase (GTP)	66.6	5.8	371.4	9	6	2	18.6
Bhyoa7455_2239	oligopeptide ABC transporter periplasmic subunit	61.3	5.9	535.2	10	10	8	21.1
Bhyoa7455_2247	hypothetical protein	25.1	4.6	258.6	6	5	3	39.9
Bhyoa7455_2257	hypothetical protein	23.3	6.4	548.9	9	8	7	44.4
Bhyoa7455_2258	hypothetical protein	21.1	6.1	184.8	4	2		26.3
Bhyoa7455_2320	extracellular solute-binding protein, family 3	30.4	4.7	1025.1	17	13		50.9
Bhyoa7455_2321	extracellular solute-binding protein, family 3	31.1	4.8	480.8	8	8		42.2
Bhyoa7455_2325	endoribonuclease	13.9	5.3	197.2	3	2		43.3
Bhyoa7455_2344	hypothetical protein	60.5	7.8	567.6	14	8	8	32.2
Bhyoa7455_2347	argininosuccinate lyase	45.6	5.6	188.7	6	4		24.9
Bhyoa7455_2357	Flagellar filament core protein flaB2	28.2	5.4	863.2	11	8	8	48.3

Bhyoa7455_2361	**variable surface protein - VspE**	**40.5**	**6.5**	**1010.1**	**14**	**13**	**9**	**41.8**
Bhyoa7455_2378	methyl-accepting chemotaxis protein McpA	67.5	4.6	342.6	8	3	2	13.7
Bhyoa7455_2381	extracellular solute-binding protein, family 5	62.3	5.0	1027.7	17	13	11	47.3
Bhyoa7455_2382	extracellular solute-binding protein, family 5	59.4	4.8	1240.8	19	17	16	42.9
Bhyoa7455_2383	extracellular solute-binding protein, family 5	60.3	4.7	435.7	10	8	7	23.1
Bhyoa7455_2404	fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB , and IIA components	77.4	6.1	909.8	19	15	12	28.1
Bhyoa7455_2411	rubrerythrin	20.6	5.9	305.7	6	3	3	32.0
Bhyoa7455_2412	superoxide dismutase	22.1	6.3	195.2	4	3		28.9
Bhyoa7455_2413	**hypothetical protein**	**38.6**	**4.4**	**164.0**	**3**	**3**	**2**	**15.3**
Bhyoa7455_2440	hypothetical protein	18.8	7.2	243.4	4	3		38.9
Bhyoa7455_2452	extracellular solute-binding protein, family 5	59.8	4.6	1276.6	25	21	18	53.2
Bhyoa7455_2465	putative preprotein translocase subunit	15.8	9.5	516.0	8	6	8	41.3
Bhyoa7455_2466	preprotein translocase subunit SecD	55.1	5.0	616.1	10	10	7	24.5
Bhyoa7455_2468	zinc finger SIM domain protein	68.3	5.1	99.1	5	2		9.6
Bhyoa7455_2477	putative flagellar basal body-associated protein	20.2	4.6	737.4	12	12	11	55.2
Bhyoa7455_2512	chemotaxis protein CheX	15.2	4.3	159.6	3	3	3	36.7
Bhyoa7455_2517	hypothetical protein	50.5	5.2	154.8	4	3		15.5
Bhyoa7455_2518	hypothetical protein	39.5	6.3	51.2	3	3		12.5
Bhyoa7455_2553	ABC-type oligopeptide transport system, periplasmic component	59.8	5.1	1509.3	28	26	21	57.8
Bhyoa7455_2554	ABC-type oligopeptide transport system, periplasmic component	61.2	5.5	385.8	9	9	7	26.7
Bhyoa7455_2574	ferrous iron transport protein B	92.3	6.0	689.5	14	13	11	21.0
Bhyoa7455_2610	hypothetical protein	22.0	9.1	318.0	7	5	4	44.6
Bhyoa7455_2618	basic membrane lipoprotein	16.9	4.2	254.5	6	4	3	52.6
Bhyoa7455_2665	**basic membrane lipoprotein**	**23.2**	**7.5**	**253.5**	**5**	**3**	**3**	**31.8**
Bhyoa7455_2670	periplasmic-iron-binding protein BitB	17.1	5.0	155.2	3	3	2	31.8
Bhyoa7455_2671	periplasmic-iron-binding protein BitA	14.8	5.1	103.2	2	2		31.6
Bhyoa7455_2679	methyl-accepting chemotaxis protein McpA	18.8	4.3	226.6	4	4	2	30.6
Bhyoa7455_2691	periplasmic-iron-binding protein BitC	12.8	7.1	204.4	4	4	2	30.4
Bhyoa7455_2694	variable surface protein - VspF	10.9	7.8	683.8	8	8	7	53.8

Bhyoa7455_2723	periplasmic-iron-binding protein BitB	8.0	4.9	100.3	3	3		44.6

Proteins detected under conventional growth conditions (BHI supplemented with 5% FCS) in B. hyodysenteriae P8544

Accession	Protein	MW [kDa]	pI	Scores	Peptides			SC
Bhyov8544_0045	arp putative ankyrin repeat-containing protein	33.7	3.8	120.7	3	2		13.5
Bhyov8544_0054	PilZ domain containing protein	28.9	5.1	176.8	4	4	3	26.3
Bhyov8544_0060	hypothetical protein	37.5	5.9	112.4	3	2		13.4
Bhyov8544_0063	invasin; Opacity protein-like surface antigens	25.0	9.4	103.5	2	2		10.2
Bhyov8544_0067	ndhD hypothetical protein	18.9	4.8	297.0	5	4	4	51.7
Bhyov8544_0070	hypothetical protein	24.7	4.8	370.7	6	4	4	40.4
Bhyov8544_0129	**hypothetical protein**	**38.4**	**8.8**	**178.8**	**5**	**3**	**3**	**20.1**
Bhyov8544_0132	**hypothetical protein**	**29.3**	**8.6**	**88.2**	**2**	**2**	**2**	**7.0**
Bhyov8544_0134	hypothetical protein	43.0	4.6	170.6	3	3	2	11.2
Bhyov8544_0143	potD spermidine/putrescine transport ATP-binding protein PotA	45.3	4.6	825.7	14	11	10	47.0
Bhyov8544_0144	ushA putative UshA protein; putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	57.2	4.8	385.9	8	7	6	26.4
Bhyov8544_0158	cstA carbon starvation protein CstA	58.6	9.7	467.1	9	5	2	23.1
Bhyov8544_0164	**TRAP transporter solute receptor, TAXI family**	**34.4**	**4.5**	**1308.0**	**21**	**15**	**13**	**58.5**
Bhyov8544_0191	hypothetical protein	15.1	9.3	296.0	4	3	3	30.1
Bhyov8544_0192	ptsN phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	31.2	5.4	636.1	8	7	7	33.1
Bhyov8544_0195	metal dependent amidohydrolase	63.9	5.0	764.8	13	4	3	32.0
Bhyov8544_0205	arp ankyrin repeat-containing protein	15.2	5.4	365.8	6	4	3	47.4
Bhyov8544_0218	hypothetical protein	30.1	9.7	213.3	4	3		17.0
Bhyov8544_0219	hypothetical protein	30.5	6.3	346.5	6	6	4	33.5
Bhyov8544_0228	hypothetical protein	11.7	5.2	224.3	5	4		41.7
Bhyov8544_0229	hypothetical protein	11.7	7.5	118.1	3	2		41.7
Bhyov8544_0230	hypothetical protein	20.3	4.4	618.9	12	12	8	42.8

Bhyov8544_0232	periplasmic ATP/GTP-binding protein	32.7	4.3	401.3	8	6	4	41.2
Bhyov8544_0254	nox DH oxidase	50.1	6.1	1013.2	17	15	14	50.7
Bhyov8544_0260	rplY 50S ribosomal protein L25/general stress protein Ctc	21.9	5.6	252.4	5	5		37.2
Bhyov8544_0270	**hypothetical protein**	**41.0**	**5.1**	**162.5**	**4**	**4**	**4**	**19.1**
Bhyov8544_0292	binding-protein-dependent transport system, membrane component	30.6	10.3	91.3	3	3		10.7
Bhyov8544_0293	binding-protein-dependent transport system, membrane component	35.5	9.8	276.1	5	4	3	17.1
Bhyov8544_0298	oppA OppA, ABC-type oligopeptide transport system, periplasmic component	60.8	4.9	924.8	17	15	11	41.9
Bhyov8544_0305	putative dynein heavy chain	42.3	4.5	1030.9	17	12	10	60.2
Bhyov8544_0315	aminodeoxychorismate lyase	38.1	9.2	453.1	9	9	4	38.8
Bhyov8544_0321	mcpB methyl-accepting chemotaxis protein McpB	75.8	4.9	317.6	5	3	3	10.6
Bhyov8544_0325	hypothetical protein	20.9	4.8	335.8	6	6	4	40.3
Bhyov8544_0355	solute binding protein-like protein	97.5	4.8	1009.2	16	13	9	27.0
Bhyov8544_0358	ptsS phosphate ABC transporter, phosphate-binding protein	27.5	4.3	519.1	8	8	7	44.5
Bhyov8544_0364	ABC-type uncharacterized transport system, periplasmic component	32.9	4.4	887.5	14	12	10	76.3
Bhyov8544_0366	**hypothetical protein**	**18.5**	**4.7**	**343.4**	**6**	**6**	**5**	**41.2**
Bhyov8544_0378	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit	48.2	9.9	157.2	3	3		9.4
Bhyov8544_0379	biotin/lipoyl attachment domain-containing protein	64.2	5.7	1497.1	27	25	21	62.8
Bhyov8544_0380	hypothetical protein	7.0	9.9	125.2	3	3	3	50.0
Bhyov8544_0417	**hypothetical protein**	**51.3**	**4.8**	**1473.0**	**25**	**7**	**14**	**49.2**
Bhyov8544_0435	tauA ABC-type nitrate/sulfonate/bicarbonate transport system	34.1	4.5	826.2	16	14	12	69.7
Bhyov8544_0445	hypothetical protein	19.7	5.5	144.4	3	2		17.4
Bhyov8544_0456	hypothetical protein	24.5	9.2	266.0	5	3	2	25.2
Bhyov8544_0479	**hypothetical protein**	**56.9**	**4.1**	**169.0**	**3**	**3**		**6.5**
Bhyov8544_0480	**hypothetical protein**	**37.0**	**4.1**	**244.5**	**5**	**4**	**4**	**15.2**
Bhyov8544_0484	nagE pts system, N-acetylglucosamine-specific iibc component	50.6	8.7	486.3	9	6	5	22.6

Bhyov8544_0493	hypothetical protein	25.7	5.4	170.0	3	2		25.8
Bhyov8544_0496	**hypothetical protein**	**73.8**	**5.2**	**477.0**	**11**	**5**	**3**	**24.3**
Bhyov8544_0521	putative positive regulator of sigma E, RseC/MucC	15.8	9.3	291.6	8	6	4	46.4
Bhyov8544_0523	TPR domain-containing protein	53.6	6.0	862.6	18	12	10	42.4
Bhyov8544_0526	**hypothetical protein**	**38.1**	**4.8**	**983.2**	**21**	**17**	**10**	**48.9**
Bhyov8544_0537	dnaK molecular chaperone DnaK	67.7	4.8	317.7	6	3		15.0
Bhyov8544_0562	fadD acyl-CoA synthetase	62.2	6.6	503.7	10	8	7	21.1
Bhyov8544_0569	carboxyl-terminal protease	55.0	5.3	246.1	4	2		11.5
Bhyov8544_0584	eno Phosphopyruvate hydratase	47.0	4.8	793.4	16	13	12	50.6
Bhyov8544_0598	amino acid-binding protein	28.6	4.9	172.0	4	2	2	13.0
Bhyov8544_0605	etfB electron transfer flavoprotein beta subunit	28.6	5.8	292.0	6	4	3	41.0
Bhyov8544_0606	acaD acyl-CoA dehydrogenase	40.0	6.1	272.6	5	5	4	21.3
Bhyov8544_0609	atpA V-type ATP synthase subunit A	65.1	5.0	198.1	4	3		11.4
Bhyov8544_0610	atpB V-type ATP synthase subunit B	48.4	4.9	184.1	4	3		12.5
Bhyov8544_0612	putative V-type ATP synthase subunit I	68.7	6.1	598.4	12	7		20.9
Bhyov8544_0622	hypothetical protein	43.1	5.1	393.3	7	5	3	26.6
Bhyov8544_0628	hypothetical protein	39.6	5.6	269.6	5	3		22.7
Bhyov8544_0630	porG pyruvate oxireductase	38.0	9.4	488.7	7	5	2	33.9
Bhyov8544_0631	porA pyruvate ferredoxin oxireductase	82.9	6.2	898.7	18	18	14	31.0
Bhyov8544_0643	hypothetical protein	23.5	5.4	370.1	6	5	2	40.8
Bhyov8544_0728	ftsY Signal recognition particle GTPase	35.4	9.1	929.9	16	14	7	49.2
Bhyov8544_0779	TPR domain-containing protein	26.2	5.5	150.4	3	3	3	16.5
Bhyov8544_0780	hypothetical protein	37.9	4.6	393.4	8	3		39.9
Bhyov8544_0782	extracellular solute-binding protein, family 5	59.7	4.6	1295.2	23	20	19	48.1
Bhyov8544_0798	hypothetical protein	33.4	5.0	210.6	4	2		22.5
Bhyov8544_0804	thrS threonyl-tRNA synthetase	73.9	5.8	363.2	6	3	3	16.3
Bhyov8544_0816	cheW purine-binding chemotaxis protein	17.9	4.3	210.1	4	3	2	32.7
Bhyov8544_0837	pep peptidase	47.1	5.3	110.0	4	3	3	7.1

Bhyov8544_0866	apbE putative thiamine biosynthesis lipoprotein apbE	37.2	4.9	147.5	3	2		13.0
Bhyov8544_0875	hypothetical protein	35.6	4.8	1048.7	19	19	14	78.1
Bhyov8544_0876	hypothetical protein	16.9	0.0	63.5	2	2		7.7
Bhyov8544_0895	OmpA family protein	25.2	9.6	265.8	5	5	3	22.6
Bhyov8544_0896	hypothetical protein	26.2	9.3	378.2	7	5	4	36.9
Bhyov8544_0897	**hypothetical protein**	**33.6**	**9.0**	**191.4**	**4**	**3**		**15.9**
Bhyov8544_0898	hypothetical protein	17.5	4.4	228.9	5	4	3	47.3
Bhyov8544_0902	fusA elongation factor G 1018293:1020329 forward MW:75343	75.3	5.1	985.6	18	12	10	36.3
Bhyov8544_0903	tufA elongation factor Tu	44.4	5.8	1190.4	24	12	12	65.7
Bhyov8544_0917	rplE 50S ribosomal protein L5	21.1	10.1	359.1	9	3		42.8
Bhyov8544_0918	rpsH 30S ribosomal protein S8	14.9	9.7	293.0	6	3		53.4
Bhyov8544_0924	secY preprotein translocase subunit SecY	49.2	10.2	177.9	6	4		16.4
Bhyov8544_0952	hypothetical protein	18.8	4.5	160.6	2	2	2	15.5
Bhyov8544_0955	**hypothetical protein**	**36.1**	**6.1**	**225.5**	**5**	**3**		**18.7**
Bhyov8544_0996	gltP GltP, Na+/H+-dicarboxylate symporter	40.2	9.2	214.2	4	3	3	13.2
Bhyov8544_1003	hypothetical protein	58.9	8.9	347.1	10	10		22.0
Bhyov8544_1024	phoB alkaline phosphatase III	57.7	4.8	679.4	13	13	11	37.7
Bhyov8544_1048	tpiA triosephosphate isomerase	27.6	5.7	230.4	3	3		17.8
Bhyov8544_1057	hypothetical protein	51.2	8.8	565.2	11	11	7	34.5
Bhyov8544_1067	glutamate synthase (DPH)	51.0	5.6	167.5	4	2		12.2
Bhyov8544_1080	vspF variable surface protein - VspF	3.6	4.1	163.1	5	4	3	71.9
Bhyov8544_1087	hypothetical protein	18.8	5.2	423.9	8	6	6	46.8
Bhyov8544_1121	hypothetical protein	38.6	4.4	137.4	3	2		15.8
Bhyov8544_1130	integral membrane transport protein	47.7	8.8	196.6	4	4	3	17.1
Bhyov8544_1139	hypothetical protein	66.2	8.5	154.0	2			9.4
Bhyov8544_1144	**hypothetical protein**	**44.1**	**5.9**	**127.5**	**4**	**3**		**10.8**

Bhyov8544_1150	rnfC electron transport complex protein	46.8	8.6	1266.2	20	16	15	49.7
Bhyov8544_1152	rnfG putative electron transport complex	19.9	4.5	729.1	11	9	8	58.6
Bhyov8544_1168	Bhyov8544_1168 hypothetical protein	39.3	5.0	165.7	4	4	4	14.7
Bhyov8544_1215	Bhyov8544_1215 hypothetical protein	40.0	4.4	769.4	12	12	10	35.3
Bhyov8544_1233	fabF 3-oxoacyl-ACP (acyl carrier protein) synthase II	44.5	6.1	167.7	4	3	3	17.3
Bhyov8544_1247	**AMP-activated protein kinase (AMPK) beta subunit glycogen binding domain (GBD)**	**29.4**	**4.8**	**132.1**	**3**	**3**	**2**	**20.9**
Bhyov8544_1254	hslJ Heat shock protein	17.2	4.1	546.8	8	8	6	37.4
Bhyov8544_1278	gatA glutamyl-tRNA(Gln) amidotransferase, A subunit	52.7	5.8	156.9	3	3	2	11.4
Bhyov8544_1297	extracellular solute-binding protein, family 5	60.8	5.1	376.5	8	6	4	19.8
Bhyov8544_1298	extracellular solute-binding protein, family 5	60.7	4.7	493.8	11	10	9	28.9
Bhyov8544_1311	tpx peroxiredoxin family, thiol peroxidase	17.9	5.2	575.5	10	8	8	70.9
Bhyov8544_1372	bitB periplasmic-iron-binding protein BitB	39.0	4.6	254.0	5	3	2	29.1
Bhyov8544_1373	bitB periplasmic-iron-binding protein BitB	38.2	4.7	389.5	8	6	4	38.1
Bhyov8544_1377	extracellular solute-binding protein, family 3	30.1	5.3	637.5	12	10	9	50.6
Bhyov8544_1387	aroB 3-dehydroquinate synthetase	39.9	6.3	58.3	3	3		6.4
Bhyov8544_1389	mglB galactose/glucose-binding protein	37.8	4.4	680.9	12	11	9	57.6
Bhyov8544_1390	mglB galactose/glucose-binding protein	38.2	4.7	2792.4	46	42	36	77.4
Bhyov8544_1391	mglA galactose/methyl galaxtoside transporter ATP-binding protein	56.1	9.1	1121.0	21	3		44.7
Bhyov8544_1411	ushA UshA, 5'-nucleotidase/2',3'-cyclic phosphodiesterase-like esterase	68.3	4.7	557.3	12	12	10	29.2
Bhyov8544_1447	anti-sigma factor antagonist	12.1	4.6	167.8	3	2	2	35.5
Bhyov8544_1473	fliF flagellar MS-ring protein	64.6	6.0	111.4	3	2		10.2
Bhyov8544_1485	ackA acetate kinase	42.8	6.7	419.6	8	4		25.6
Bhyov8544_1489	ABC transporter, transmembrane region	73.3	9.3	204.5	6	3		14.5
Bhyov8544_1500	groEL chaperonin GroEL	58.2	4.9	1252.8	19	15	12	53.6
Bhyov8544_1522	putative Na+/phosphate symporter	61.9	6.3	554.8	10	8	5	25.5

Bhyov8544_1529	mcpB methyl-accepting chemotaxis protein McpB	68.3	4.7	146.1	4	3		9.3
Bhyov8544_1600	biopolymer transport protein ExbB	22.5	5.0	136.8	5	4	3	24.3
Bhyov8544_1609	modA ModA, ABC-type molybdate transport system, periplasmic component	28.5	4.6	202.2	3	2		17.1
Bhyov8544_1626	gldG ABC-type uncharacterized transport system	61.4	9.4	626.3	11	5		29.9
Bhyov8544_1635	tar8 putative methyl-accepting chemotaxis protein	74.0	4.4	681.0	15	7	5	30.5
Bhyov8544_1637	cheY chemotaxis response regulator CheY	13.5	7.6	317.1	5	4	3	45.9
Bhyov8544_1642	cheB response regulator receiver modulated CheB methylesterase	41.0	9.0	451.9	7	6		32.3
Bhyov8544_1649	Bhyov8544_1649 undefined product	47.0	9.6	136.7	2			5.1
Bhyov8544_1661	lmp1 TPR domain-containing protein	52.5	5.1	1027.3	21	20	13	55.2
Bhyov8544_1662	tsf elongation factor Ts	31.2	5.2	234.3	6	5	2	28.2
Bhyov8544_1663	rpsB 30S ribosomal protein S2	29.6	5.0	421.2	10	7	5	44.7
Bhyov8544_1670	oppA ABC-type oligopeptide transport system, periplasmic component	60.7	4.7	1095.5	20	20	18	48.1
Bhyov8544_1696	bmpB BmpB, outer membrane lipoprotein	29.7	4.3	691.6	11	11	10	36.9
Bhyov8544_1705	hypothetical protein	19.3	5.2	380.7	7	6	4	55.6
Bhyov8544_1732	**hypothetical protein**	**60.6**	**5.9**	**1135.5**	**22**	**20**	**18**	**47.1**
Bhyov8544_1738	hypothetical protein	27.5	5.0	337.5	7	3	3	38.1
Bhyov8544_1748	iars isoleucyl-tRNA synthetase	106.0	5.8	172.3	5	4	4	7.6
Bhyov8544_1760	cheY chemotaxis protein CheY	15.6	9.2	223.2	4	3	3	32.4
Bhyov8544_1764	mreB rod shape-determining protein mreB 1988191:1989195 forward MW:35924	35.9	5.5	228.4	4	3	3	25.1
Bhyov8544_1779	hppA membrane-bound proton-translocating pyrophosphatase	79.9	5.9	782.2	13	8	8	23.2
Bhyov8544_1799	outer membrane protein	100.3	6.7	1316.7	23	15	12	34.4
Bhyov8544_1837	**acetyltransferase, GT family**	**20.9**	**5.2**	**111.5**	**4**	**3**		**5.7**
Bhyov8544_1851	hypothetical protein	27.3	4.8	101.6	3	3		14.0
Bhyov8544_1861	acetyl-CoA acetyltransferase	40.9	8.8	448.2	8	6		30.1
Bhyov8544_1862	crt 3-hydroxybutyryl-CoA dehydratase	27.7	5.4	292.9	6	5	4	35.7
Bhyov8544_1863	crt 3-hydroxybutyryl-CoA dehydratase	29.9	8.8	391.8	7	5	4	36.4

Bhyov8544_1866	rsxE SoxR-reducing system protein RsxE	23.4	10.0	139.2	2	2		5.0
Bhyov8544_1867	rnfA RnfA, Predicted DH:ubiquinone oxidoreductase, subunit RnfA	21.1	9.4	105.8	2	2		5.7
Bhyov8544_1868	ferredoxin	29.6	9.4	557.2	14	10	3	60.4
Bhyov8544_1894	aspC aspartate aminotransferase	45.8	5.8	307.7	7	2		31.9
Bhyov8544_1921	basic membrane lipoprotein 2168784:2169836 forward MW:38616	38.6	4.6	315.2	8	6	3	37.7
Bhyov8544_1922	**basic membrane lipoprotein**	**36.9**	**4.6**	**853.6**	**14**	**13**	**11**	**52.6**
Bhyov8544_1931	hypothetical protein	10.0	5.4	270.9	7	6	4	48.9
Bhyov8544_1937	amino acid transport system permease protein	26.3	9.4	220.8	4	4		18.1
Bhyov8544_1938	extracellular solute-binding protein, family 3	29.2	4.5	1686.6	22	21	19	52.9
Bhyov8544_1944	lea hypothetical protein	18.4	9.3	523.3	8	8	7	51.5
Bhyov8544_1966	spoIIAA SpoIIAA, Anti-anti-sigma regulatory factor	12.2	5.2	145.4	3	2		26.4
Bhyov8544_1973	**vspE variable surface protein - VspE**	**40.5**	**6.5**	**533.3**	**11**	**6**	**4**	**32.9**
Bhyov8544_1986	extracellular solute-binding protein, family 5	40.0	4.7	97.5	2	2		10.8
Bhyov8544_1987	hypothetical protein	11.8	6.1	262.3	6	5	3	53.3
Bhyov8544_1995	aspS aspartyl-tRNA synthetase	66.9	5.2	187.3	4	3		13.0
Bhyov8544_2002	**hypothetical protein**	**15.5**	**9.5**	**158.4**	**2**	**2**		**18.6**
Bhyov8544_2009	ompA outer membrane protein	22.6	9.4	147.1	5	4		39.4
Bhyov8544_2010	ompA OmpA family protein	23.9	4.6	381.1	7	6	5	51.2
Bhyov8544_2034	motB putative flagellar motor protein	28.9	7.5	174.6	4	3	3	25.9
Bhyov8544_2035	motA Flagellar Motor Protein	27.8	4.8	682.3	10	8	8	43.7
Bhyov8544_2044	extracellular solute-binding protein, family 5	61.8	4.9	2338.2	42	38	37	63.9
Bhyov8544_2064	hypothetical protein	28.1	4.6	454.7	7	7	3	46.1
Bhyov8544_2071	Zn dependant metalloprotease	25.8	9.1	246.7	5	4	2	23.3
Bhyov8544_2075	hypothetical protein	60.5	8.4	464.1	8	5	5	18.9
Bhyov8544_2078	argH argininosuccinate lyase	45.6	5.6	333.0	8	6	3	31.8
Bhyov8544_2103	prolipoprotein diacylglyceryl transferase	35.8	9.5	129.6	2	2		10.6
Bhyov8544_2129	hypothetical protein	26.8	5.0	865.9	16	1	15	58.1

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Bhyov8544_2147	**arp ankyrin repeat-containing protein**	**61.1**	**4.3**	**767.1**	**13**	**11**	**10**	**38.6**
Bhyov8544_2152	**hypothetical protein**	**59.3**	**4.8**	**313.1**	**7**	**6**		**13.3**
Bhyov8544_2169	hypothetical protein	15.5	7.1	138.0	2	2		17.6
Bhyov8544_2171	periplasmic solute binding protein	32.3	4.6	339.6	6	4	3	27.2
Bhyov8544_2173	**vspA variable surface protein A**	**38.1**	**4.5**	**648.1**	**9**	**9**	**8**	**37.9**
Bhyov8544_2176	ABC transporter substrate binding protein 2	35.1	4.6	1003.1	16	15	9	54.7
Bhyov8544_2184	hypothetical protein	30.7	4.5	1172.0	20	16	10	54.6
Bhyov8544_2185	**hypothetical protein**	**58.0**	**4.9**	**682.0**	**14**	**8**	**6**	**31.3**
Bhyov8544_2186	**hypothetical protein**	**59.1**	**4.8**	**487.2**	**9**	**7**	**5**	**21.6**
Bhyov8544_2190	secA preprotein translocase, SecA subunit	111.0	5.9	739.6	13	9		20.4
Bhyov8544_2193	bitC periplasmic-iron-binding protein BitC	8.4	7.1	222.4	4	3	3	56.8
Bhyov8544_2199	hypothetical protein	23.3	6.4	484.5	7	4	4	38.3
Bhyov8544_2209	hypothetical protein	25.1	4.5	310.1	6	3		33.6
Bhyov8544_2217	oppA oligopeptide ABC transporter periplasmic subunit	61.3	5.9	593.1	12	7	6	26.1
Bhyov8544_2228	arp ankyrin repeat-containing protein	43.3	4.6	217.1	6	2		18.3
Bhyov8544_2234	pgi glucose-6-phosphate isomerase	49.5	6.4	162.8	4	3		14.9
Bhyov8544_2264	undefined product	16.8	9.9	143.9	2	2		22.0
Bhyov8544_2279	rubrerythrin fusion protein	20.4	5.4	317.7	6	6	5	51.6
Bhyov8544_2321	basic membrane lipoprotein	17.9	4.2	246.7	6	4	3	54.7
Bhyov8544_2341	hypothetical protein	11.0	9.1	122.0	3	2		19.1
Bhyov8544_2345	extracellular solute-binding protein, family 5	60.3	4.7	590.0	12	9	8	31.6
Bhyov8544_2346	extracellular solute-binding protein, family 5	59.4	4.8	1336.0	19	18	17	47.0
Bhyov8544_2347	extracellular solute-binding protein, family 5	62.3	5.0	935.6	16	13	10	43.1
Bhyov8544_2348	hypothetical protein	47.8	4.3	170.0	3	3		11.4
Bhyov8544_2372	glyceraldehyde-3-phosphate dehydrogenase	38.1	7.8	469.5	11	10	9	35.2
Bhyov8544_2373	pgk phosphoglycerate kinase	44.1	5.8	608.4	13	12	8	46.7

Bhyov8544_2387	hypothetical protein	50.0	5.0	338.0	8	3	2	24.6
Bhyov8544_2403	arp ankyrin repeat-containing protein	40.7	4.3	673.2	13	9	8	42.0
Bhyov8544_2407	cutF lipoprotein involved with copper homeostasis and adhesion	14.7	4.0	178.1	2	2	2	26.0
Bhyov8544_2417	**hypothetical protein**	**28.2**	**5.5**	**287.6**	**5**	**5**	**5**	**25.2**
Bhyov8544_2426	phosphoenolpyruvate carboxykinase (GTP)	66.7	5.8	333.3	7	7	5	21.6
Bhyov8544_2437	extracellular solute-binding protein, family 3	30.4	4.7	1228.5	18	16	14	47.3
Bhyov8544_2438	extracellular solute-binding protein, family 3	31.1	4.8	444.5	8	7	7	42.5
Bhyov8544_2442	endoribonuclease	13.9	5.3	384.8	5	5	3	51.2
Bhyov8544_2464	2750623:2752782 forward MW:77416	77.4	6.1	612.2	12	9	9	22.9
Bhyov8544_2468	hypothetical protein	55.9	9.2	314.5	5	5	3	15.3
Bhyov8544_2471	rbr rubrerythrin	20.6	5.9	572.3	11	9	7	64.0
Bhyov8544_2472	sodA superoxide dismutase	22.1	6.3	296.4	6	4	4	35.6
Bhyov8544_2483	undefined product	53.4	5.4	75.4	3	3		10.6
Bhyov8544_2485	MoxR-like ATPase	38.5	5.1	369.0	8	7		33.4
Bhyov8544_2501	hypothetical protein	77.0	4.9	620.0	10	5		19.1
Bhyov8544_2511	iron-containing alcohol dehydrogenase	42.0	5.5	541.4	10	8	5	36.8
Bhyov8544_2549	fliL putative flagellar basal body-associated protein	20.2	4.6	719.9	13	12	11	60.2
Bhyov8544_2559	secF preprotein translocase	34.3	8.8	327.0	5	4	4	24.4
Bhyov8544_2560	secD preprotein translocase subunit SecD	55.1	5.0	696.2	12	12	11	27.0
Bhyov8544_2561	yajC putative preprotein translocase subunit	15.8	9.5	593.2	9	9	7	39.2
Bhyov8544_2610	oppA ABC-type oligopeptide transport system, periplasmic component	59.8	5.1	1145.7	22	19	18	46.9
Bhyov8544_2636	hypothetical protein	85.6	5.5	272.8	6	4		13.6
Bhyov8544_2648	hypothetical protein	50.0	4.7	273.2	6	5	3	15.8
Bhyov8544_2659	hypothetical protein	14.9	4.5	287.0	4	3	3	22.9
Bhyov8544_2672	bitB periplasmic-iron-binding protein BitB	35.6	4.8	541.7	10	6	5	43.2
Bhyov8544_2696	bitC periplasmic-iron-binding protein BitC	24.3	4.8	289.7	6	4	3	42.9
Bhyov8544_2713	**vspF variable surface protein - VspF**	**14.1**	**9.6**	**1168.2**	**20**	**18**	**18**	**77.3**
Bhyov8544_2731	bitB periplasmic-iron-binding protein BitB	10.0	9.0	298.6	6	5	3	69.9

Lipoproteins predicted by SpLiP

Proteins with beta-barrel predicted by BOMP